

701049\_sequence\_listing.txt  
SEQUENCE LISTING

<110> Yamanaka, Shinya  
Dainippon Sumitomo Pharma Co., Ltd.

<120> Screening method for somatic cell nuclear reprogramming substance

<130> 701049

<150> JP 2004-042337

<151> 2004-02-19

<150> JP 2004-232961

<151> 2004-08-10

<150> JP 2004-276572

<151> 2004-09-24

<160> 50

<170> PatentIn Ver. 2.1

<210> 1

<211> 1623

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (50)..(1369)

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Leu Lys Arg Phe Gln Thr Leu Val Pro Leu Asp His Lys Gln Gly Thr  
5 10 15

tta ttt gaa att att gga gag ccc aag ttg ccc aag tgg ttc cat gtc 154  
Leu Phe Glu Ile Ile Gly Glu Pro Lys Leu Pro Lys Trp Phe His Val  
20 25 30 35

gaa tgc ctg gaa gat cca aaa aga ctg tac gtg gaa cct cgg cta ctg 202  
Glu Cys Leu Glu Asp Pro Lys Arg Leu Tyr Val Glu Pro Arg Leu Leu  
40 45 50

gaa atc atg ttt ggt aag gat gga gag cac atc cca cat ctt gaa tct 250  
Glu Ile Met Phe Gly Lys Asp Gly Glu His Ile Pro His Leu Glu Ser  
55 60 65

atg ttg cac acc ctg ata cat gtg aac gtg tgg ggc cct gaa agg cga 298  
Met Leu His Thr Leu Ile His Val Asn Val Trp Gly Pro Glu Arg Arg  
70 75 80

gct gag att tgg ata ttc gga ccg ccg cct ttc cga agg gac gtt gac 346  
Ala Glu Ile Trp Ile Phe Gly Pro Pro Pro Phe Arg Arg Asp Val Asp  
85 90 95

cgg atg ctc act gat ctg gct cac tat tgc cgc atg aaa ctg atg gaa 394  
Arg Met Leu Thr Asp Leu Ala His Tyr Cys Arg Met Lys Leu Met Glu  
100 105 110 115

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ata gag gct ctg gag gct gga gtt gag cgt cgt cgt atg gcg gcc cat	442
Ile Glu Ala Leu Glu Ala Gly Val Glu Arg Arg Arg Met Ala Ala His	
	120
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Lys Ala Ala Thr Gln Pro Ala Pro Val Lys Val Arg Glu Ala Ala Pro	
	135
cgg ccc gct tcc gtg aag gtc cct gag acg gcc acc cag cct gct ccc	538
Arg Pro Ala Ser Val Lys Val Pro Glu Thr Ala Thr Gln Pro Ala Pro	
	150
gtg aag gtc cgc gag gct gcc cct cag ccc gct ccg gtg cag gag gtc	586
Val Lys Val Arg Glu Ala Ala Pro Gln Pro Ala Pro Val Gln Glu Val	
	165
cgc gag gct gcc cct cag cag gct tcc gtg cag gag gag gtc cgc gag	634
Arg Glu Ala Ala Pro Gln Gln Ala Ser Val Gln Glu Glu Val Arg Glu	
	180
gct gcc acc gag cag gct ccc gtg cag gag gtc cgc gag gct gcc acc	682
Ala Ala Thr Glu Gln Ala Pro Val Gln Glu Val Arg Glu Ala Ala Thr	
	200
gag cag gct ccc gtg cag gag gtc agc gag gct gcc acc gag cag gct	730
Glu Gln Ala Pro Val Gln Glu Val Ser Glu Ala Ala Thr Glu Gln Ala	
	215
ccc gtg cag gag gtc aac gag gct gcc acc gag cag gct tcc gtg cag	778
Pro Val Gln Glu Val Asn Glu Ala Ala Thr Glu Gln Ala Ser Val Gln	
	230
gcg gtc cgc gag gct gcc acc cgg ccg gct ccc ggg aag gtc cgc aag	826
Ala Val Arg Glu Ala Ala Thr Arg Pro Ala Pro Gly Lys Val Arg Lys	
	245
gcg gcc acc cag ccg gct ccg gtg cag gtt tgc cag gag gcc acc cag	874
Ala Ala Thr Gln Pro Ala Pro Val Gln Val Cys Gln Glu Ala Thr Gln	
	260
ttg gct ccc gtg aag gtc cgc gag gcg gcc acc cag ccg gct tcc ggg	922
Leu Ala Pro Val Lys Val Arg Glu Ala Ala Thr Gln Pro Ala Ser Gly	
	280
aag gtc cgc gag gcg gcc acc cag ttg gct cct gtg aag gtc cgc aag	970
Lys Val Arg Glu Ala Ala Thr Gln Leu Ala Pro Val Lys Val Arg Lys	
	295
gca gcc acc cag ttg gct cct gtg aag gtc cac gag gcg gcc acc cag	1018
Ala Ala Thr Gln Leu Ala Pro Val Lys Val His Glu Ala Ala Thr Gln	
	310
ccg gct ccg ggg aag gtc agc gat gct gcc acg cag tcg gct tcg gtg	1066
Pro Ala Pro Gly Lys Val Ser Asp Ala Ala Thr Gln Ser Ala Ser Val	
	325
cag gtt cgt gag gct gcc acg cag ctg tct ccc gtg gag gcc act gat	1114
Gln Val Arg Glu Ala Ala Thr Gln Leu Ser Pro Val Glu Ala Thr Asp	
	340
act agc cag ttg gct cag gtg aag gct gat gaa gcc ttt gcc cag cac	1162
Thr Ser Gln Leu Ala Gln Val Lys Ala Asp Glu Ala Phe Ala Gln His	

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360

365

370

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act tca ggg gag gcc cac cag gtt gcc aat ggg cag tct ccc att gaa 1210
Thr Ser Gly Glu Ala His Gln Val Ala Asn Gly Gln Ser Pro Ile Glu
375 380 385

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Val Cys Glu Thr Ala Thr Gly Gln His Ser Leu Asp Val Ser Arg Ala
390 395 400

ttg tcc cag aag tgt cct gag gtt ttt gag tgg gag acc cag agt tgt 1306
Leu Ser Gln Lys Cys Pro Glu Val Phe Glu Trp Glu Thr Gln Ser Cys
405 410 415

ttg gat ggc agc tat gtc ata gtt cag cct cca agg gat gcc tgg gaa 1354
Leu Asp Gly Ser Tyr Val Ile Val Gln Pro Pro Arg Asp Ala Trp Glu
420 425 430 435

tca ttt atc ata tta taaatgcatc tctggtgtga gccaggatag atggtacacg 1409
Ser Phe Ile Ile Leu
440

tctgcaaatc cagaacctaa aggcaggggt tagcttgggc tgagtaaggc aatgatctta 1469
aacctcagcc tgcctaagac tcccttcac tttctttctg gtttttgccc taggaatcgg 1529
gaagaacaga gtagagctgt ttttgtttcc ccattgtgtt aaatgtttgc agacacaatt 1589
taaagtattc taataaaaaa aaaattgcat tccc 1623

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<210> 2  
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 <212> PRT  
 <213> Mus musculus

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Phe His Val Glu Cys Leu Glu Asp Pro Lys Arg Leu Tyr Val Glu Pro
35 40 45

Arg Leu Leu Glu Ile Met Phe Gly Lys Asp Gly Glu His Ile Pro His
50 55 60

Leu Glu Ser Met Leu His Thr Leu Ile His Val Asn Val Trp Gly Pro
65 70 75 80

Glu Arg Arg Ala Glu Ile Trp Ile Phe Gly Pro Pro Pro Phe Arg Arg
85 90 95

Asp Val Asp Arg Met Leu Thr Asp Leu Ala His Tyr Cys Arg Met Lys
100 105 110

Leu Met Glu Ile Glu Ala Leu Glu Ala Gly Val Glu Arg Arg Arg Met
115 120 125

Ala Ala His Lys Ala Ala Thr Gln Pro Ala Pro Val Lys Val Arg Glu
130 135 140

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Ala Ala Pro Arg Pro Ala Ser Val Lys Val Pro Glu Thr Ala Thr Gln  
145 150 155 160  
Pro Ala Pro Val Lys Val Arg Glu Ala Ala Pro Gln Pro Ala Pro Val  
165 170 175  
Gln Glu Val Arg Glu Ala Ala Pro Gln Gln Ala Ser Val Gln Glu Glu  
180 185 190  
Val Arg Glu Ala Ala Thr Glu Gln Ala Pro Val Gln Glu Val Arg Glu  
195 200 205  
Ala Ala Thr Glu Gln Ala Pro Val Gln Glu Val Ser Glu Ala Ala Thr  
210 215 220  
Glu Gln Ala Pro Val Gln Glu Val Asn Glu Ala Ala Thr Glu Gln Ala  
225 230 235 240  
Ser Val Gln Ala Val Arg Glu Ala Ala Thr Arg Pro Ala Pro Gly Lys  
245 250 255  
Val Arg Lys Ala Ala Thr Gln Pro Ala Pro Val Gln Val Cys Gln Glu  
260 265 270  
Ala Thr Gln Leu Ala Pro Val Lys Val Arg Glu Ala Ala Thr Gln Pro  
275 280 285  
Ala Ser Gly Lys Val Arg Glu Ala Ala Thr Gln Leu Ala Pro Val Lys  
290 295 300  
Val Arg Lys Ala Ala Thr Gln Leu Ala Pro Val Lys Val His Glu Ala  
305 310 315 320  
Ala Thr Gln Pro Ala Pro Gly Lys Val Ser Asp Ala Ala Thr Gln Ser  
325 330 335  
Ala Ser Val Gln Val Arg Glu Ala Ala Thr Gln Leu Ser Pro Val Glu  
340 345 350  
Ala Thr Asp Thr Ser Gln Leu Ala Gln Val Lys Ala Asp Glu Ala Phe  
355 360 365  
Ala Gln His Thr Ser Gly Glu Ala His Gln Val Ala Asn Gly Gln Ser  
370 375 380  
Pro Ile Glu Val Cys Glu Thr Ala Thr Gly Gln His Ser Leu Asp Val  
385 390 395 400  
Ser Arg Ala Leu Ser Gln Lys Cys Pro Glu Val Phe Glu Trp Glu Thr  
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Gln Ser Cys Leu Asp Gly Ser Tyr Val Ile Val Gln Pro Pro Arg Asp  
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Ala Trp Glu Ser Phe Ile Ile Leu  
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<210> 3  
<211> 1063  
<212> DNA

## 701049\_sequence\_listing.txt

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54)..(704)

&lt;400&gt; 3

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Asp Ala Pro Arg 5 Arg Phe Pro Thr Leu Val Gln Leu Met Gln Pro Lys	15
gca atg cca gtg gag gtg ctc ggt cac ctc cct aag cgg ttc tcc tgg	152
Ala Met Pro Val 20 Glu Val Leu Gly 25 His Leu Pro Lys Arg 30 Phe Ser Trp	
ttc cac tct gag ttc ctg aag aat ccg aag gta gtt cgc ctt gag gtt	200
Phe His 35 Ser Glu Phe Leu Lys 40 Asn Pro Lys Val Val 45 Arg Leu Glu Val	
tgg ctg gtg gaa aag atc ttc ggc cgg ggc gga gaa cgc atc ccg cac	248
Trp Leu Val 50 Glu Lys 55 Ile Phe Gly Arg Gly 60 Glu Arg Ile Pro His 65	
gtc cag ggt atg tcc caa atc ttg att cac gtg aat cga ttg gac cct	296
Val Gln Gly Met 70 Gln Ile Leu Ile His 75 Val Asn Arg Leu Asp 80 Pro	
aac ggc gag gct gag atc ttg gta ttt ggg agg cct tct tac cag gag	344
Asn Gly Glu 85 Ala Glu Ile Leu Val Phe 90 Gly Arg Pro Ser Tyr 95 Gln Glu	
gac aca atc aag atg atc atg aac ctg gct gac tat cac cgc cag ctc	392
Asp Thr 100 Ile Lys Met Ile Met Asn 105 Leu Ala Asp Tyr His 110 Arg Gln Leu	
cag gcg aaa ggc tca gga aag gcc ctc gcc cag gat gtc gcc act cag	440
Gln Ala 115 Lys Gly Ser Gly Lys 120 Ala Leu Ala Gln Asp 125 Val Ala Thr Gln	
aag gcc gag acc cag cgg tct tca ata gaa gtc cgg gag gcc ggg acg	488
Lys Ala 130 Glu Thr Gln Arg 135 Ser Ser Ile Glu Val 140 Arg Glu Ala Gly Thr 145	
cag cgt tcg gtg gag gtc cgg gag gcc ggg acc cag cgt tcg gtg gaa	536
Gln Arg Ser Val 150 Glu Val Arg Glu Ala Gly 155 Thr Gln Arg Ser Val 160 Glu	
gtc cag gag gtc ggg aca cag ggt tct ccg gtg gag gtg cag gag gcc	584
Val Gln Glu Val 165 Gly Thr Gln Gly Ser 170 Pro Val Glu Val 175 Gln Glu Ala	
ggg acc cag cag tct ctc cag gct gcc aac aag tcg ggg acc cag cga	632
Gly Thr 180 Gln Gln Ser Leu Gln Ala 185 Ala Asn Lys Ser Gly 190 Thr Gln Arg	
tcc ccc gaa gct gcc agc aag gca gtg acc cag cgg ttt cgc gag gat	680
Ser Pro 195 Glu Ala Ala Ser Lys 200 Ala Val Thr Gln Arg 205 Phe Arg Glu Asp	

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gcc cgg gac cca gtt act aga tta tgaaggcatc tcaggccctg gagccagagc 734
Ala Arg Asp Pro Val Thr Arg Leu
210 215

cagtcagggg ttaaagtgaag agcccgtatt tccgcccaga agctgggggtt ggggagagga 794
tgtggatttt ttgttttacc ctttctgttg catggttgca aacacaaact tgagttctaa 854
taaagaattg caaagtggaa gcccgcctcc cccctccccc ccgcctccct taagtccagg 914
aagctgggggt ggcgaggaag gatgatgtgg attgtttttg ttttaccctt tttgttgaat 974
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<210> 4
<211> 217
<212> PRT
<213> Homo sapiens

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 20 25 30
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 35 40 45
Val Trp Leu Val Glu Lys Ile Phe Gly Arg Gly Gly Glu Arg Ile Pro
 50 55 60
His Val Gln Gly Met Ser Gln Ile Leu Ile His Val Asn Arg Leu Asp
 65 70 75 80
Pro Asn Gly Glu Ala Glu Ile Leu Val Phe Gly Arg Pro Ser Tyr Gln
 85 90 95
Glu Asp Thr Ile Lys Met Ile Met Asn Leu Ala Asp Tyr His Arg Gln
 100 105 110
Leu Gln Ala Lys Gly Ser Gly Lys Ala Leu Ala Gln Asp Val Ala Thr
 115 120 125
Gln Lys Ala Glu Thr Gln Arg Ser Ser Ile Glu Val Arg Glu Ala Gly
 130 135 140
Thr Gln Arg Ser Val Glu Val Arg Glu Ala Gly Thr Gln Arg Ser Val
 145 150 155 160
Glu Val Gln Glu Val Gly Thr Gln Gly Ser Pro Val Glu Val Gln Glu
 165 170 175
Ala Gly Thr Gln Gln Ser Leu Gln Ala Ala Asn Lys Ser Gly Thr Gln
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<220>  
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 <222> (59)..(412)

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 Met Met Val Thr Leu Val Thr Arg Lys Asp Ile Pro Pro Trp Val Lys  
 1 5 10 15  
 gtt cct gaa gac ctg aaa gat cca gaa gta ttc cag gtc cag tcg ctg 154  
 Val Pro Glu Asp Leu Lys Asp Pro Glu Val Phe Gln Val Gln Ser Leu  
 20 25 30  
 gtg ctg aaa tat ctg ttt ggc cca cag gga tct cga atg tct cac atc 202  
 Val Leu Lys Tyr Leu Phe Gly Pro Gln Gly Ser Arg Met Ser His Ile  
 35 40 45  
 gag cag gtg agc cag gcc atg ttt gag ctg aag aac ctg gaa tct ccc 250  
 Glu Gln Val Ser Gln Ala Met Phe Glu Leu Lys Asn Leu Glu Ser Pro  
 50 55 60  
 gaa gaa ctt atc gag gtc ttc att tac ggc tct caa aac aac aag att 298  
 Glu Glu Leu Ile Glu Val Phe Ile Tyr Gly Ser Gln Asn Asn Lys Ile  
 65 70 75 80  
 cgg gct aaa tgg atg ctt cag tcc atg gct gag agg tac cac ctg cgc 346  
 Arg Ala Lys Trp Met Leu Gln Ser Met Ala Glu Arg Tyr His Leu Arg  
 85 90 95  
 cag caa aaa gga gtg ctg aag ctg gag gaa tcc atg aag acc ctg gag 394  
 Gln Gln Lys Gly Val Leu Lys Leu Glu Glu Ser Met Lys Thr Leu Glu  
 100 105 110  
 cta ggc cag tgt atc gag tgaagccagt ttccagtcct tgtgtctccg 442  
 Leu Gly Gln Cys Ile Glu  
 115  
 acctggatgc aggttaagct gtggccagt tttggttctg gcgggatttt tagctttggt 502  
 acatcctagc aagatattct ggatccctgc tgcgcattct gatgtgaatc ccaaggttac 562  
 cactctaaat aaaaaataaa attgaagtg 591

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 <212> PRT  
 <213> Mus musculus

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Val Leu Lys<sub>35</sub> Tyr Leu Phe Gly Pro<sub>40</sub> Gln Gly Ser Arg Met<sub>45</sub> Ser His Ile  
Glu Gln<sub>50</sub> Val Ser Gln Ala Met<sub>55</sub> Phe Glu Leu Lys Asn<sub>60</sub> Leu Glu Ser Pro  
Glu Glu Leu Ile Glu Val<sub>70</sub> Phe Ile Tyr Gly Ser<sub>75</sub> Gln Asn Asn Lys Ile<sub>80</sub>  
Arg Ala Lys Trp Met<sub>85</sub> Leu Gln Ser Met Ala<sub>90</sub> Glu Arg Tyr His Leu<sub>95</sub> Arg  
Gln Gln Lys Gly<sub>100</sub> Val Leu Lys Leu Glu<sub>105</sub> Glu Ser Met Lys Thr<sub>110</sub> Leu Glu  
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<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (15) .. (362)

[illegible]



## 701049\_sequence\_listing.txt

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acccttggtt ctgagtcctt ttgtgaatat ttctttgatg attgttaata aaaagtgttt 572  
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aaaaaaaaa 640

<210> 8  
<211> 116  
<212> PRT  
<213> Homo sapiens

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20 25 30  
Leu Lys Ala Ile Phe Gly Pro Asp Gly Ser Arg Ile Pro Tyr Ile Glu  
35 40 45  
Gln Val Ser Lys Ala Met Leu Glu Leu Lys Ala Leu Glu Ser Ser Asp  
50 55 60  
Leu Thr Glu Val Val Val Tyr Gly Ser Tyr Leu Tyr Lys Leu Arg Thr  
65 70 75 80  
Lys Trp Met Leu Gln Ser Met Ala Glu Trp His Arg Gln Arg Gln Glu  
85 90 95  
Arg Gly Met Leu Lys Leu Ala Glu Ala Met Asn Ala Leu Glu Leu Gly  
100 105 110  
Pro Trp Met Lys  
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<210> 9  
<211> 1670  
<212> DNA  
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<220>  
<221> CDS  
<222> (134)..(1567)

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tgaggagtaca ata atg gag gag tcg gaa ttg gag att ttt aga agt aag 169  
Met Glu Glu Ser Glu Leu Glu Ile Phe Arg Ser Lys  
1 5 10

## 217

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## 701049\_sequence\_listing.txt

255	260	265	
gtg ggg ctg tgg cag gag aat ggt gga cta gct ttt gtc atg gca aat Val Gly Leu Trp Gln Glu Asn Gly Gly Leu Ala Phe Val Met Ala Asn 270 275 280			985
att cat tcc cat ggc ctt ttc gag aga agc ata atg ggc tca gac act Ile His Ser His Gly Leu Phe Glu Arg Ser Ile Met Gly Ser Asp Thr 285 290 295 300			1033
att ccc tat aca ttg cct ccc gac act aca ttt gtg gat aac tac cca Ile Pro Tyr Thr Leu Pro Pro Asp Thr Thr Phe Val Asp Asn Tyr Pro 305 310 315			1081
gac tca atg acc ttt tat gga gat aaa ggc ttt cag ctg cat atc gac Asp Ser Met Thr Phe Tyr Gly Asp Lys Gly Phe Gln Leu His Ile Asp 320 325 330			1129
att cat ggc agt aag act tac ttc ctg tgt agc acc ttc cac aat ctc Ile His Gly Ser Lys Thr Tyr Phe Leu Cys Ser Thr Phe His Asn Leu 335 340 345			1177
ttc tgc agg aga gcg ggc att aac aat gga tat gtg aag ttc ttg atg Phe Cys Arg Arg Ala Gly Ile Asn Asn Gly Tyr Val Lys Phe Leu Met 350 355 360			1225
ata aac tta aaa aat aac aga gaa cac cta cct ctt gtt gga aaa gtt Ile Asn Leu Lys Asn Asn Arg Glu His Leu Pro Leu Val Gly Lys Val 365 370 375 380			1273
ggc ctt gaa tgg aga act gac tgt tta aat ggc cgt att gag agt tgc Gly Leu Glu Trp Arg Thr Asp Cys Leu Asn Gly Arg Ile Glu Ser Cys 385 390 395			1321
att gta gtg gat atg acc ttg ctg gat gag gac aag aag ccc atc tgg Ile Val Val Asp Met Thr Leu Leu Asp Glu Asp Lys Lys Pro Ile Trp 400 405 410			1369
tat gtg agt tct cca gtg tgc ttg aga tct gcc tgc ctt cct gat ttc Tyr Val Ser Ser Pro Val Cys Leu Arg Ser Ala Cys Leu Pro Asp Phe 415 420 425			1417
ccg cag ccg gct tac tct ttc gag tac atg gac agc gta gga gga gtg Pro Gln Pro Ala Tyr Ser Phe Glu Tyr Met Asp Ser Val Gly Gly Val 430 435 440			1465
tgc gca gac cta ggg tgg ttt gaa aat acc gat gaa tac ttc att gtc Cys Ala Asp Leu Gly Trp Phe Glu Asn Thr Asp Glu Tyr Phe Ile Val 445 450 455 460			1513
aga ctg gac att tac ctc agt gta gca aaa tta caa caa tgg ttt ggg Arg Leu Asp Ile Tyr Leu Ser Val Ala Lys Leu Gln Gln Trp Phe Gly 465 470 475			1561
agg caa taaatgctga gtttagcagta gggagtccttg ttattagtaa gctgtttgtt Arg Gln			1617
ttttacaact ttgttttttat tgaaagttaa aataaagcat atttgtggta ttc			1670

<210> 10  
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 <212> PRT

## 701049\_sequence\_listing.txt

&lt;213&gt; Mus musculus

&lt;400&gt; 10

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Ser 70 Ser 75 Val 80 Thr 85 Lys 90 Gln 95 His 100 Ala 105 Trp 110 Arg 115 Asn 120 Gln 125 His 130 Ser 135 Glu 140 Lys
Arg 145 Cys 150 Ser 155 Ser 160 Ile 165 Ser 170 Ser 175 Ile 180 Ser 185 Leu 190 Asp 195 Arg 200 Met 205 Pro 210 Ser
Glu 215 Ile 220 Leu 225 Val 230 Lys 235 Ile 240 Leu 245 Ser 250 Ile 255 Leu 260 Val 265 Thr 270 Ala 275 Val 280 Thr 285
Cys 290 Ile 295 Gly 300 Cys 305 Val 310 Ser 315 Arg 320 Arg 325 Phe 330 Tyr 335 His 340 Leu 345 Ala 350 Asp 355 Asp 360 Asn
Leu 365 Ile 370 Trp 375 Val 380 Arg 385 Lys 390 Tyr 395 Ala 400 Ala 405 Phe 410 Arg 415 Ser 420 Lys 425 Arg 430 Ser
Arg 435 Trp 440 Lys 445 Ala 450 Thr 455 Ser 460 Val 465 Glu 470 Glu 475 Thr 480 Ala 485 Thr 490 Ser 495 Leu 500 Ser 505
Leu 510 Ser 515 Val 520 Trp 525 Asp 530 Lys 535 Glu 540 Asp 545 Tyr 550 Trp 555 Lys 560 Lys 565 Glu 570 Tyr 575 Ile
Thr 580 Lys 585 Gln 590 Ile 595 Ser 600 Ser 605 Val 610 Arg 615 Ala 620 Ala 625 Leu 630 Thr 635 Asn 640 Ser 645 Leu 650 Ser
Pro 655 Val 660 Lys 665 Arg 670 Arg 675 Thr 680 Ser 685 Leu 690 Pro 695 Ser 700 Lys 705 Thr 710 Lys 715 Glu 720 Ser 725 Leu
Arg 730 Ile 735 Ser 740 Gly 745 Leu 750 Gly 755 Trp 760 Thr 765 Ile 770 Ile 775 Leu 780 Arg 785 Glu 790 Ala 795 Ser 800 Gly
Lys 805 Glu 810 His 815 Ile 820 Met 825 Gln 830 His 835 Ser 840 Asn 845 Leu 850 Ser 855 Val 860 Asn 865 Asp 870 Asn 875 Ser
Val 880 Thr 885 Val 890 Phe 895 Trp 900 His 905 Asp 910 Lys 915 Asn 920 Trp 925 Pro 930 His 935 Val 940 Asp 945 Thr 950 Leu
Ser 955 Thr 960 Leu 965 Asp 970 Leu 975 Tyr 980 Gly 985 Ala 990 Thr 995 Pro 1000 Ile 1005 Phe 1010 Met 1015 Glu 1020 Gln 1025 Tyr
Lys 1030 Gly 1035 Pro 1040 Asn 1045 Thr 1050 Ser 1055 Cys 1060 Pro 1065 Arg 1070 Trp 1075 Leu 1080 Ser 1085 Leu 1090 Ile 1095 Glu 1100 Lys
Tyr 1105 Asp 1110 Leu 1115 Ser 1120 Asn 1125 Leu 1130 Arg 1135 Lys 1140 Ser 1145 Ala 1150 Met 1155 Ile 1160 Gly 1165 Cys 1170 Asp 1175 Arg
His 1180 Val 1185 Arg 1190 Val 1195 Phe 1200 Cys 1205 Val 1210 Asn 1215 Pro 1220 Gly 1225 Leu 1230 Leu 1235 Val 1240 Gly 1245 Leu 1250 Trp
Gln 1255 Glu 1260 Asn 1265 Gly 1270 Gly 1275 Leu 1280 Ala 1285 Phe 1290 Val 1295 Met 1300 Ala 1305 Asn 1310 Ile 1315 His 1320 Ser 1325 His
Gly 1330 Leu 1335 Phe 1340 Glu 1345 Arg 1350 Ser 1355 Ile 1360 Met 1365 Gly 1370 Ser 1375 Asp 1380 Thr 1385 Ile 1390 Pro 1395 Tyr 1400 Thr
Leu 1405 Pro 1410 Pro 1415 Asp 1420 Thr 1425 Thr 1430 Phe 1435 Val 1440 Asp 1445 Asn 1450 Tyr 1455 Pro 1460 Asp 1465 Ser 1470 Met 1475 Thr
305 310 315 320

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701049\_sequence\_listing.txt

Phe Tyr Gly Asp Lys Gly Phe Gln Leu His Ile Asp Ile His Gly Ser  
 325 330 335  
 Lys Thr Tyr Phe Leu Cys Ser Thr Phe His Asn Leu Phe Cys Arg Arg  
 340 345 350  
 Ala Gly Ile Asn Asn Gly Tyr Val Lys Phe Leu Met Ile Asn Leu Lys  
 355 360 365  
 Asn Asn Arg Glu His Leu Pro Leu Val Gly Lys Val Gly Leu Glu Trp  
 370 375 380  
 Arg Thr Asp Cys Leu Asn Gly Arg Ile Glu Ser Cys Ile Val Val Asp  
 385 390 395 400  
 Met Thr Leu Leu Asp Glu Asp Lys Lys Pro Ile Trp Tyr Val Ser Ser  
 405 410 415  
 Pro Val Cys Leu Arg Ser Ala Cys Leu Pro Asp Phe Pro Gln Pro Ala  
 420 425 430  
 Tyr Ser Phe Glu Tyr Met Asp Ser Val Gly Gly Val Cys Ala Asp Leu  
 435 440 445  
 Gly Trp Phe Glu Asn Thr Asp Glu Tyr Phe Ile Val Arg Leu Asp Ile  
 450 455 460  
 Tyr Leu Ser Val Ala Lys Leu Gln Gln Trp Phe Gly Arg Gln  
 465 470 475

<210> 11  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (21)..(1550)

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 Met Ala Thr Gly Arg Gly Arg Ile Leu Gln Gln  
 1 5 10  
 cac tgg ctc ggc ctc cag acg ctg cgc ggg ccc agc agg ggc ggt ggc 101  
 His Trp Leu Gly Leu Gln Thr Leu Arg Gly Pro Ser Arg Gly Gly Gly  
 15 20 25  
 gcg gcc cgg ggg cgc gcc agg gcc ttt ggg tgc aga aag ggg cca ggg 149  
 Ala Ala Arg Gly Arg Ala Arg Ala Phe Gly Cys Arg Lys Gly Pro Gly  
 30 35 40  
 gtc aag ctt tct gca ggc tct gct gcc ctg agg tgc cat gcc gga ggt 197  
 Val Lys Leu Ser Ala Gly Ser Ala Ala Leu Arg Cys His Ala Gly Gly  
 45 50 55  
 gga cag cac tgg gag agc tct ttc tcc tgc tgt tct ggg ttc ctg gat 245  
 Gly Gln His Trp Glu Ser Ser Phe Ser Cys Cys Ser Gly Phe Leu Asp  
 60 65 70 75  
 gga atg cct tca gaa atc ttg ctg aag ata ttt tcc tac ttg gat gct 293

## 701049\_sequence\_listing.txt

Gly	Met	Pro	Ser	Glu	Ile	Leu	Leu	Lys	Ile	Phe	Ser	Tyr	Leu	Asp	Ala		
				80					85					90			
gtg	agc	ctt	ctg	tgt	act	gga	tgt	gtg	agc	agg	cgc	ttt	tat	cat	cta	341	
Val	Ser	Leu	Leu	Cys	Thr	Gly	Cys	Val	Ser	Arg	Arg	Phe	Tyr	His	Leu		
			95					100				105					
gcc	aat	gac	aat	ttt	att	tgg	atc	gga	atc	tac	tca	act	gct	ttt	tca	389	
Ala	Asn	Asp	Asn	Phe	Ile	Trp	Ile	Gly	Ile	Tyr	Ser	Thr	Ala	Phe	Ser		
		110					115					120					
cct	gca	aga	tca	aat	tgg	aaa	ttt	aat	tca	gta	gag	aag	ata	gct	atg	437	
Pro	Ala	Arg	Ser	Asn	Trp	Lys	Phe	Asn	Ser	Val	Glu	Lys	Ile	Ala	Met		
	125					130					135						
tct	atg	agc	ttt	ctg	tca	gtt	cag	gat	aaa	gaa	gct	ggt	tat	tgg	aag	485	
Ser	Met	Ser	Phe	Leu	Ser	Val	Gln	Asp	Lys	Glu	Ala	Gly	Tyr	Trp	Lys		
	140				145					150					155		
aaa	gaa	tat	atc	aca	aaa	caa	ata	gca	tct	gta	aaa	gcc	gca	cta	gct	533	
Lys	Glu	Tyr	Ile	Thr	Lys	Gln	Ile	Ala	Ser	Val	Lys	Ala	Ala	Leu	Ala		
				160				165						170			
gac	att	ctc	aaa	cct	gtc	aac	cct	tac	aca	ggc	ctt	cca	gtt	aag	acc	581	
Asp	Ile	Leu	Lys	Pro	Val	Asn	Pro	Tyr	Thr	Gly	Leu	Pro	Val	Lys	Thr		
			175					180					185				
aaa	gag	gcc	ctc	aga	ata	ttt	ggt	tta	ggt	tgg	gca	att	ata	ctg	aaa	629	
Lys	Glu	Ala	Leu	Arg	Ile	Phe	Gly	Leu	Gly	Trp	Ala	Ile	Ile	Leu	Lys		
		190					195					200					
gaa	aaa	ggt	gga	aaa	gaa	tat	atc	atg	gag	cat	gtt	gat	ctt	tcc	ata	677	
Glu	Lys	Gly	Gly	Lys	Glu	Tyr	Ile	Met	Glu	His	Val	Asp	Leu	Ser	Ile		
	205					210					215						
aat	gac	aca	tca	gtt	act	gtt	ata	tgg	tat	ggc	aaa	aaa	tgg	cca	tgc	725	
Asn	Asp	Thr	Ser	Val	Thr	Val	Ile	Trp	Tyr	Gly	Lys	Lys	Trp	Pro	Cys		
	220				225					230					235		
cta	gca	tca	ttg	tca	acc	tta	gat	tta	tgt	ggc	atg	aca	cca	gtt	ttt	773	
Leu	Ala	Ser	Leu	Ser	Thr	Leu	Asp	Leu	Cys	Gly	Met	Thr	Pro	Val	Phe		
				240					245					250			
acc	gac	tgg	tat	aaa	act	ccc	acc	aaa	cat	aga	ctc	cga	tgg	cat	tct	821	
Thr	Asp	Trp	Tyr	Lys	Thr	Pro	Thr	Lys	His	Arg	Leu	Arg	Trp	His	Ser		
			255					260					265				
tta	att	gca	aag	tac	aat	ctg	agt	cat	ttg	acc	ata	tct	acc	atg	att	869	
Leu	Ile	Ala	Lys	Tyr	Asn	Leu	Ser	His	Leu	Thr	Ile	Ser	Thr	Met	Ile		
		270				275						280					
ggc	tgt	gac	aga	ctc	att	cgg	atc	ttc	tgc	ctg	cac	cct	ggc	ctc	ctg	917	
Gly	Cys	Asp	Arg	Leu	Ile	Arg	Ile	Phe	Cys	Leu	His	Pro	Gly	Leu	Leu		
	285					290					295						
gtg	gga	gtg	tgg	aag	aag	gag	gaa	gaa	ctg	gct	ttt	gtt	atg	gca	aat	965	
Val	Gly	Val	Trp	Lys	Lys	Glu	Glu	Glu	Leu	Ala	Phe	Val	Met	Ala	Asn		
					305					310					315		
ctt	cat	ttt	cat	cac	ctt	gtg	gag	agg	agc	aca	tta	ggc	tcg	gct	act	1013	
Leu	His	Phe	His	His	Leu	Val	Glu	Arg	Ser	Thr	Leu	Gly	Ser	Ala	Thr		
				320					325					330			

## 701049\_sequence\_listing.txt

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atc ccc tat gaa ctg cct cca cat agc ccc ttt ttg gat gat agc ccc 1061
Ile Pro Tyr Glu Leu Pro Pro His Ser Pro Phe Leu Asp Asp Ser Pro
335 340 345

gag tat gga ctg cac ggc tac caa ctc cat gtt gat ctg cac agc ggt 1109
Glu Tyr Gly Leu His Gly Tyr Gln Leu His Val Asp Leu His Ser Gly
350 355 360

ggg gtt ttc tac cta tgt ggt aca ttt cgc aat ctc ttc acc aag aga 1157
Gly Val Phe Tyr Leu Cys Gly Thr Phe Arg Asn Leu Phe Thr Lys Arg
365 370 375

gga aat att gaa aat gga cat gtg aag ctc att gtt ata cat tta aaa 1205
Gly Asn Ile Glu Asn Gly His Val Lys Leu Ile Val Ile His Leu Lys
380 385 390

aat aac aga gaa cac cta cct ctt att gga aaa gtt ggc ctc tcg tgg 1253
Asn Asn Arg Glu His Leu Pro Leu Ile Gly Lys Val Gly Leu Ser Trp
400 405 410

aaa act gat att ttt gat ggc tgt ata aag agt tgt tcc atg atg gac 1301
Lys Thr Asp Ile Phe Asp Gly Cys Ile Lys Ser Cys Ser Met Met Asp
415 420 425

gta act ctt ttg gat gaa cat ggg aaa ccc ttt tgg tgt ttc agt tcc 1349
Val Thr Leu Leu Asp Glu His Gly Lys Pro Phe Trp Cys Phe Ser Ser
430 435 440

ccg gtg tgc ctg aga tcg cct gcc aca ccc tct gac agc tct agc ttc 1397
Pro Val Cys Leu Arg Ser Pro Ala Thr Pro Ser Asp Ser Ser Ser Phe
445 450 455

ttg gga cag aca tac aac gtg gac tac gtt gat gcg gaa gga aga gtg 1445
Leu Gly Gln Thr Tyr Asn Val Asp Tyr Val Asp Ala Glu Gly Arg Val
460 465 470 475

cac gtg gag ctg gtg tgg atc aga gag acc gaa gaa tac ctt att gtc 1493
His Val Glu Leu Val Trp Ile Arg Glu Thr Glu Glu Tyr Leu Ile Val
480 485 490

aac ctg gtc ctt tat ctt agt atc gca aaa atc aac cat tgg ttt ggg 1541
Asn Leu Val Leu Tyr Leu Ser Ile Ala Lys Ile Asn His Trp Phe Gly
495 500 505

act gaa tat tagcagtagg tggcaaatta ttgttggttat ttagttgttt 1590
Thr Glu Tyr
510

atttttgact ggctttgttc ttggtgttga aaattaaaat aaagcaaadc tgcaaaaaaa 1650
aaaaaaaaaa aaaaaa 1665

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<210> 12  
 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Ala Thr Gly Arg Gly Arg Ile Leu Gln Gln His Trp Leu Gly Leu  
 1 5 10 15

Gln Thr Leu Arg Gly Pro Ser Arg Gly Gly Gly Ala Ala Arg Gly Arg  
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701049\_sequence\_listing.txt

20

25

30

Ala Arg Ala Phe Gly Cys Arg Lys Gly Pro Gly Val Lys Leu Ser Ala  
35 40 45  
Gly Ser Ala Ala Leu Arg Cys His Ala Gly Gly Gly Gln His Trp Glu  
50 55 60  
Ser Ser Phe Ser Cys Cys Ser Gly Phe Leu Asp Gly Met Pro Ser Glu  
65 70 75 80  
Ile Leu Leu Lys Ile Phe Ser Tyr Leu Asp Ala Val Ser Leu Leu Cys  
85 90 95  
Thr Gly Cys Val Ser Arg Arg Phe Tyr His Leu Ala Asn Asp Asn Phe  
100 105 110  
Ile Trp Ile Gly Ile Tyr Ser Thr Ala Phe Ser Pro Ala Arg Ser Asn  
115 120 125  
Trp Lys Phe Asn Ser Val Glu Lys Ile Ala Met Ser Met Ser Phe Leu  
130 135 140  
Ser Val Gln Asp Lys Glu Ala Gly Tyr Trp Lys Lys Glu Tyr Ile Thr  
145 150 155 160  
Lys Gln Ile Ala Ser Val Lys Ala Ala Leu Ala Asp Ile Leu Lys Pro  
165 170 175  
Val Asn Pro Tyr Thr Gly Leu Pro Val Lys Thr Lys Glu Ala Leu Arg  
180 185 190  
Ile Phe Gly Leu Gly Trp Ala Ile Ile Leu Lys Glu Lys Gly Gly Lys  
195 200 205  
Glu Tyr Ile Met Glu His Val Asp Leu Ser Ile Asn Asp Thr Ser Val  
210 215 220  
Thr Val Ile Trp Tyr Gly Lys Lys Trp Pro Cys Leu Ala Ser Leu Ser  
225 230 235 240  
Thr Leu Asp Leu Cys Gly Met Thr Pro Val Phe Thr Asp Trp Tyr Lys  
245 250 255  
Thr Pro Thr Lys His Arg Leu Arg Trp His Ser Leu Ile Ala Lys Tyr  
260 265 270  
Asn Leu Ser His Leu Thr Ile Ser Thr Met Ile Gly Cys Asp Arg Leu  
275 280 285  
Ile Arg Ile Phe Cys Leu His Pro Gly Leu Leu Val Gly Val Trp Lys  
290 295 300  
Lys Glu Glu Glu Leu Ala Phe Val Met Ala Asn Leu His Phe His His  
305 310 315 320  
Leu Val Glu Arg Ser Thr Leu Gly Ser Ala Thr Ile Pro Tyr Glu Leu  
325 330 335  
Pro Pro His Ser Pro Phe Leu Asp Asp Ser Pro Glu Tyr Gly Leu His  
340 345 350  
Gly Tyr Gln Leu His Val Asp Leu His Ser Gly Gly Val Phe Tyr Leu



701049\_sequence\_listing.txt

355

360

365

Cys Gly Thr Phe Arg Asn Leu Phe Thr Lys Arg Gly Asn Ile Glu Asn  
 370 375 380  
 Gly His Val Lys Leu Ile Val Ile His Leu Lys Asn Asn Arg Glu His  
 385 390 395 400  
 Leu Pro Leu Ile Gly Lys Val Gly Leu Ser Trp Lys Thr Asp Ile Phe  
 405 410 415  
 Asp Gly Cys Ile Lys Ser Cys Ser Met Met Asp Val Thr Leu Leu Asp  
 420 425 430  
 Glu His Gly Lys Pro Phe Trp Cys Phe Ser Ser Pro Val Cys Leu Arg  
 435 440 445  
 Ser Pro Ala Thr Pro Ser Asp Ser Ser Ser Phe Leu Gly Gln Thr Tyr  
 450 455 460  
 Asn Val Asp Tyr Val Asp Ala Glu Gly Arg Val His Val Glu Leu Val  
 465 470 475 480  
 Trp Ile Arg Glu Thr Glu Glu Tyr Leu Ile Val Asn Leu Val Leu Tyr  
 485 490 495  
 Leu Ser Ile Ala Lys Ile Asn His Trp Phe Gly Thr Glu Tyr  
 500 505 510

<210> 13

<211> 2184

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (190)..(1104)

<400> 13

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 tagacactga gttttttggg tgttgcctaa aaccttttca gaaatccctt ccctcgccat 180  
 cacactgac atg agt gtg ggt ctt cct ggt ccc cac agt ttg cct agt tct 231  
 Met Ser Val Gly Leu Pro Gly Pro His Ser Leu Pro Ser Ser  
 1 5 10  
 gag gaa gca tcg aat tct ggg aac gcc tca tca atg cct gca gtt ttt 279  
 Glu Glu Ala Ser Asn Ser Gly Asn Ala Ser Ser Met Pro Ala Val Phe  
 15 20 25 30  
 cat ccc gag aac tat tct tgc tta caa ggg tct gct act gag atg ctc 327  
 His Pro Glu Asn Tyr Ser Cys Leu Gln Gly Ser Ala Thr Glu Met Leu  
 35 40 45  
 tgc aca gag gct gcc tct cct cgc cct tcc tct gaa gac ctg cct ctt 375  
 Cys Thr Glu Ala Ala Ser Pro Arg Pro Ser Ser Glu Asp Leu Pro Leu  
 50 55 60

## 701049\_sequence\_listing.txt

caa ggc agc cct gat tct tct acc agt ccc aaa caa aag ctc tca agt	423
Gln Gly Ser 65 Pro Asp Ser Ser Thr 70 Ser Pro Lys Gln Lys 75 Leu Ser Ser	
cct gag gct gac aag ggc cct gag gag gag gag aac aag gtc ctt gcc	471
Pro Glu Ala Asp Lys Gly Pro 85 Glu Glu Glu Glu Asn 90 Lys Val Leu Ala	
agg aag cag aag atg cgg act gtg ttc tct cag gcc cag ctg tgt gca	519
Arg Lys Gln Lys Met Arg Thr Val Phe Ser Gln Ala Gln Leu Cys Ala 110	
ctc aag gac agg ttt cag aag cag aag tac ctc agc ctc cag cag atg	567
Leu Lys Asp Arg Phe 115 Gln Lys Gln Lys Tyr 120 Leu Ser Leu Gln Gln Met	
caa gaa ctc tcc tcc att ctg aac ctg agc tat aag cag gtt aag acc	615
Gln Glu Leu Ser 130 Ile Leu Asn 135 Ser Tyr Lys Gln Val 140 Lys Thr	
tgg ttt caa aac caa agg gtg aag tgc aag cgg tgg cag aaa aac cag	663
Trp Phe Gln Asn Gln Arg Val Lys 150 Cys Lys Arg Trp 155 Gln Lys Asn Gln	
tgg ttg aag act agc aat ggt ctg att cag aag ggc tca gca cca gtg	711
Trp Leu Lys Thr Ser Asn Gly 165 Leu Ile Gln Lys Gly 170 Ser Ala Pro Val	
gag tat ccc agc atc cat tgc agc tat ccc cag ggc tat ctg gtg aac	759
Glu Tyr Pro Ser Ile His 180 Cys Ser Tyr Pro Gln Gly Tyr Leu Val Asn 190	
gca tct gga agc ctt tcc atg tgg ggc agc cag act tgg acc aac cca	807
Ala Ser Gly Ser Leu Ser Met Trp Gly Ser 200 Gln Thr Trp Thr Asn 205 Pro	
act tgg agc agc cag acc tgg acc aac cca act tgg aac aac cag acc	855
Thr Trp Ser Ser Gln Thr Trp Thr Asn 215 Pro Thr Trp Asn Asn 220 Gln Thr	
tgg acc aac cca act tgg agc agc cag gcc tgg acc gct cag tcc tgg	903
Trp Thr Asn Pro Thr Trp Ser Ser Gln Ala Trp Thr Ala Gln Ser Trp	
aac ggc cag cct tgg aat gct gct ccg ctc cat aac ttc ggg gag gac	951
Asn Gly Gln Pro Trp Asn Ala 245 Ala Pro Leu His Asn 250 Phe Gly Glu Asp	
ttt ctg cag cct tac gta cag ttg cag caa aac ttc tct gcc agt gat	999
Phe Leu Gln Pro Tyr Val 260 Gln Leu Gln Gln Asn 265 Phe Ser Ala Ser Asp 270	
ttg gag gtg aat ttg gaa gcc act agg gaa agc cat gcg cat ttt agc	1047
Leu Glu Val Asn 275 Glu Ala Thr Arg Glu Ser His Ala His Phe Ser	
acc cca caa gcc ttg gaa tta ttc ctg aac tac tct gtg act cca cca	1095
Thr Pro Gln Ala Leu Glu Leu Phe Leu 295 Asn Tyr Ser Val Thr 300 Pro Pro	
ggt gaa ata tgagacttac gcaacatctg ggcttaaagt cagggcaaag	1144
Gly Glu Ile 305	

701049\_sequence\_listing.txt

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ccagggttcct tccttcttcc aaatattttc atattttttt taaagattta tttattcatt 1204
atatgtaagt acactgtagc tgtcttcaga cactccagaa gagggcgta gatcttgta 1264
cgtatggttg tgagccacca tgtggttgct gggatttgaa ctctgacct tcggaagagc 1324
agtcgggtgc tcttatccac tgagccatct caccagcccc tggtttattt ttttaattat 1384
tatttgcttt ttgtttatca agacaggggt tctctgcata gctctaattg tctttgaact 1444
agctctgcag accagcctgg ccttgaactc agagatctgc ccacttatct ttgcctcctg 1504
aatgctggga ccaaagggtg cataccacca cacctggcat atatattggt tatttctatt 1564
tctattttta ttggtgccag agcaaacctt ggacttagaa catgctgggc accaactcaa 1624
cttctgagct ctattttaca cttggtgtgt tagtgtattt gtcttagttc tgaatttgtc 1684
cttttttttag tgtaactctt aggccttgga gacagtgagg tgcataactt ctctccttcc 1744
caagaataag tgcttgaaca cccttaccct cgtccaccca cccatgctag tcttttttct 1804
tagaagcgtg ggtcttggtt tacactgtgt cattttgagg ggtgaggttt aaaagtatat 1864
acaaagtata acgatatggt ggctactctc gaggatgaga cagaaggacc aggagtttga 1924
gggtagctca gatatgcaat aagttcaagg ccaacctgta ctatgtttta atagtaagac 1984
agcatctcga taaaataata aaactaaagt ctcaacaaaa taaaagcttt cacctattaa 2044
ggtgcttgct tgccttgga gtccccaag agtaactgct atgttaatat ctgtagaaaag 2104
atgtttatat ttgactgtac catgatgaac cgatgccagc tggactagtt taaacaaaat 2164
aaaacactaa ttttaccttt                                     2184

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<210> 14  
 <211> 305  
 <212> PRT  
 <213> Mus musculus

<400> 14  
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 Ala Ser Asn Ser Gly Asn Ala Ser Ser Met Pro Ala Val Phe His Pro  
 20 25 30  
 Glu Asn Tyr Ser Cys Leu Gln Gly Ser Ala Thr Glu Met Leu Cys Thr  
 35 40 45  
 Glu Ala Ala Ser Pro Arg Pro Ser Ser Glu Asp Leu Pro Leu Gln Gly  
 50 55 60  
 Ser Pro Asp Ser Ser Thr Ser Pro Lys Gln Lys Leu Ser Ser Pro Glu  
 65 70 75 80  
 Ala Asp Lys Gly Pro Glu Glu Glu Glu Asn Lys Val Leu Ala Arg Lys  
 85 90 95  
 Gln Lys Met Arg Thr Val Phe Ser Gln Ala Gln Leu Cys Ala Leu Lys  
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701049\_sequence\_listing.txt

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100                               105                               110
Asp Arg Phe Gln Lys Gln Lys Tyr Leu Ser Leu Gln Gln Met Gln Glu
115                               120                               125
Leu Ser Ser Ile Leu Asn Leu Ser Tyr Lys Gln Val Lys Thr Trp Phe
130                               135                               140
Gln Asn Gln Arg Val Lys Cys Lys Arg Trp Gln Lys Asn Gln Trp Leu
145                               150                               155
Lys Thr Ser Asn Gly Leu Ile Gln Lys Gly Ser Ala Pro Val Glu Tyr
165                               170
Pro Ser Ile His Cys Ser Tyr Pro Gln Gly Tyr Leu Val Asn Ala Ser
180                               185                               190
Gly Ser Leu Ser Met Trp Gly Ser Gln Thr Trp Thr Asn Pro Thr Trp
195                               200                               205
Ser Ser Gln Thr Trp Thr Asn Pro Thr Trp Asn Asn Gln Thr Trp Thr
210                               215                               220
Asn Pro Thr Trp Ser Ser Gln Ala Trp Thr Ala Gln Ser Trp Asn Gly
225                               230                               235
Gln Pro Trp Asn Ala Ala Pro Leu His Asn Phe Gly Glu Asp Phe Leu
245                               250                               255
Gln Pro Tyr Val Gln Leu Gln Gln Asn Phe Ser Ala Ser Asp Leu Glu
260                               265                               270
Val Asn Leu Glu Ala Thr Arg Glu Ser His Ala His Phe Ser Thr Pro
275                               280                               285
Gln Ala Leu Glu Leu Phe Leu Asn Tyr Ser Val Thr Pro Pro Gly Glu
290                               295                               300
Ile
305

```

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<210> 15
<211> 2114
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (217)..(1131)

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tatttctcta acatcttcca gaaaagtctt aaagctgcct taaccttttt tccagtccac 180
ctcttaaatt ttttcctcct cttcctctat actaac atg agt gtg gat cca gct 234
Met Ser Val Asp Pro Ala
1 5

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## 701049\_sequence\_listing.txt

tgt ccc caa agc ttg cct tgc ttt gaa gca tcc gac tgt aaa gaa tct	282
Cys Pro Gln Ser 10 Leu Pro Cys Phe Glu 15 Ala Ser Asp Cys Lys 20 Glu Ser	
tca cct atg cct gtg att tgt ggg cct gaa gaa aac tat cca tcc ttg	330
Ser Pro Met 25 Pro Val Ile Cys Gly 30 Pro Glu Glu Asn Tyr 35 Pro Ser Leu	
caa atg tct tct gct gag atg cct cac acg gag act gtc tct cct ctt	378
Gln Met 40 Ser Ser Ala Glu Met 45 Pro His Thr Glu Thr 50 Val Ser Pro Leu	
ccc tcc tcc atg gat ctg ctt att cag gac agc cct gat tct tcc acc	426
Pro Ser Ser Met Asp Leu 60 Leu Ile Gln Asp Ser 65 Pro Asp Ser Ser Thr 70	
agt ccc aaa ggc aaa caa ccc act tct gca gag aat agt gtc gca aaa	474
Ser Pro Lys Gly 75 Gln Pro Thr Ser Ala 80 Glu Asn Ser Val Ala 85 Lys	
aag gaa gac aag gtc cca gtc aag aaa cag aag acc aga act gtg ttc	522
Lys Glu Asp Lys 90 Val Pro Val Lys Lys 95 Gln Lys Thr Arg Thr 100 Val Phe	
tct tcc acc cag ctg tgt gta ctc aat gat aga ttt cag aga cag aaa	570
Ser Ser Thr 105 Gln Leu Cys Val Leu 110 Asn Asp Arg Phe Gln 115 Arg Gln Lys	
tac ctc agc ctc cag cag atg caa gaa ctc tcc aac atc ctg aac ctc	618
Tyr Leu 120 Ser Leu Gln Gln Met 125 Gln Glu Leu Ser Asn 130 Ile Leu Asn Leu	
agc tac aaa cag gtg aag acc tgg ttc cag aac cag aga atg aaa tct	666
Ser Tyr Lys Gln Val Lys 140 Thr Trp Phe Gln Asn Gln Arg Met Lys 150 Ser	
aag agg tgg cag aaa aac aac tgg ccg aag aat agc aat ggt gtg acg	714
Lys Arg Trp Gln Lys 155 Asn Asn Trp Pro Lys 160 Asn Ser Asn Gly Val 165 Thr	
cag aag gcc tca gca cct acc tac ccc agc ctc tac tct tcc tac cac	762
Gln Lys Ala Ser 170 Ala Pro Thr Tyr Pro 175 Ser Leu Tyr Ser Ser 180 Tyr His	
cag gga tgc ctg gtg aac ccg act ggg aac ctt cca atg tgg agc aac	810
Gln Gly Cys 185 Leu Val Asn Pro Thr 190 Gly Asn Leu Pro Met 195 Trp Ser Asn	
cag acc tgg aac aat tca acc tgg agc aac cag acc cag aac atc cag	858
Gln Thr 200 Trp Asn Asn Ser Thr 205 Trp Ser Asn Gln Thr 210 Gln Asn Ile Gln	
tcc tgg agc aac cac tcc tgg aac act cag acc tgg tgc acc caa tcc	906
Ser Trp Ser Asn His Ser 220 Trp Asn Thr Gln Thr 225 Trp Cys Thr Gln Ser 230	
tgg aac aat cag gcc tgg aac agt ccc ttc tat aac tgt gga gag gaa	954
Trp Asn Asn Gln Ala 235 Trp Asn Ser Pro Phe 240 Tyr Asn Cys Gly 245 Glu Glu	
tct ctg cag tcc tgc atg cag ttc cag cca aat tct cct gcc agt gac	1002
Ser Leu Gln Ser 250 Cys Met Gln Phe 255 Gln Pro Asn Ser Pro Ala 260 Ser Asp	

701049\_sequence\_listing.txt

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ttg gag gct gct ttg gaa gct gct ggg gaa ggc ctt aat gta ata cag 1050
Leu Glu Ala Ala Leu Glu Ala Ala Gly Glu Gly Leu Asn Val Ile Gln
      265                270                275

cag acc act agg tat ttt agt act cca caa acc atg gat tta ttc cta 1098
Gln Thr Thr Arg Tyr Phe Ser Thr Pro Gln Thr Met Asp Leu Phe Leu
      280                285                290

aac tac tcc atg aac atg caa cct gaa gac gtg tgaagatgag tgaaactgat 1151
Asn Tyr Ser Met Asn Met Gln Pro Glu Asp Val
      295                300                305

attactcaat ttcagtctgg acactggctg aatccttcct ctcccctcct cccatccctc 1211

ataggatttt tcttgtttgg aaaccacgtg ttctggtttc catgatgcct atccagtcaa 1271

tctcatggag ggtggagtat ggttggagcc taatcagcga ggtttctttt tttttttttc 1331

ctattggatc ttcctggaga aaatactttt tttttttttt ttgagacgga gtcttgctct 1391

gtcgcccagg ctggagtgca gtggcgcggt cttggctcac tgcaagctcc gcctcccggg 1451

ttcacgccat tctcctgcct cagcctcccg agcagctggg actacaggcg cccgccacct 1511

cgcccggcta atattttgta tttttagtag agacagggtt tctctgtgtt agccaggatg 1571

gtctcgatct cctgaccttg tgatccgccc gcctcggcct ccctaacagc tgggattaca 1631

ggcgtgagcc accgcgccct gcctagaaaa gacattttta taaccttggc tgctaaggac 1691

aacattgata gaagccgtct ctggctatag ataagtagat ctaatactag tttggatatc 1751

tttagggttt agaatctaac ctcaagaata agaaatacaa gtacgaattg gtgatgaaga 1811

tgtattcgta ttgtttggga ttgggaggct ttgcttattt ttttaaaact attgaggtaa 1871

aggggttaagc tgtaacatac ttaattgatt tcttaccgtt tttggctctg ttttgctata 1931

tcccctaatt tgttggttgt gctaattctt gtagaaagag gtcttgtatt tgctgcatcg 1991

taatgacatg agtactactt tagttggttt aagttcaaat gaatgaaaca aatatttttc 2051

ctttagttga ttttaccctg atttcaccga gtgtttcgat gagtaaatat acagcttaaa 2111

cat 2114

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<210> 16  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Ser Val Asp Pro Ala Cys Pro Gln Ser Leu Pro Cys Phe Glu Ala  
 1 5 10 15  
 Ser Asp Cys Lys Glu Ser Ser Pro Met Pro Val Ile Cys Gly Pro Glu  
 20 25 30  
 Glu Asn Tyr Pro Ser Leu Gln Met Ser Ser Ala Glu Met Pro His Thr  
 35 40 45

## 701049\_sequence\_listing.txt

Glu Thr Val Ser Pro Leu Pro Ser Ser Met Asp Leu Leu Ile Gln Asp  
 50 55 60  
 Ser Pro Asp Ser Ser Thr Ser Pro Lys Gly Lys Gln Pro Thr Ser Ala  
 65 70 75 80  
 Glu Asn Ser Val Ala Lys Lys Glu Asp Lys Val Pro Val Lys Lys Gln  
 85 90 95  
 Lys Thr Arg Thr Val Phe Ser Ser Thr Gln Leu Cys Val Leu Asn Asp  
 100 105 110  
 Arg Phe Gln Arg Gln Lys Tyr Leu Ser Leu Gln Gln Met Gln Glu Leu  
 115 120 125  
 Ser Asn Ile Leu Asn Leu Ser Tyr Lys Gln Val Lys Thr Trp Phe Gln  
 130 135 140  
 Asn Gln Arg Met Lys Ser Lys Arg Trp Gln Lys Asn Asn Trp Pro Lys  
 145 150 155 160  
 Asn Ser Asn Gly Val Thr Gln Lys Ala Ser Ala Pro Thr Tyr Pro Ser  
 165 170 175  
 Leu Tyr Ser Ser Tyr His Gln Gly Cys Leu Val Asn Pro Thr Gly Asn  
 180 185 190  
 Leu Pro Met Trp Ser Asn Gln Thr Trp Asn Asn Ser Thr Trp Ser Asn  
 195 200 205  
 Gln Thr Gln Asn Ile Gln Ser Trp Ser Asn His Ser Trp Asn Thr Gln  
 210 215 220  
 Thr Trp Cys Thr Gln Ser Trp Asn Asn Gln Ala Trp Asn Ser Pro Phe  
 225 230 235 240  
 Tyr Asn Cys Gly Glu Glu Ser Leu Gln Ser Cys Met Gln Phe Gln Pro  
 245 250 255  
 Asn Ser Pro Ala Ser Asp Leu Glu Ala Ala Leu Glu Ala Ala Gly Glu  
 260 265 270  
 Gly Leu Asn Val Ile Gln Gln Thr Thr Arg Tyr Phe Ser Thr Pro Gln  
 275 280 285  
 Thr Met Asp Leu Phe Leu Asn Tyr Ser Met Asn Met Gln Pro Glu Asp  
 290 295 300  
 Val  
 305

<210> 17  
 <211> 1078  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (178)..(858)

<400> 17

## 701049\_sequence\_listing.txt

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caggggtcgg gcaggtggga gggggaagct cacatctccg ccctctgctg cctctggggg 60
tagggagcat cctaaccccc aactgtccgg tcagatccgc ctactgcccc tcatcagact 120
gctactcctg ggagcacagc acctgtcttt tacacctctt ccttgagctg ctggggga 177
atg gct ttg cct aca aag tct agc atc ttg gac ctg agc tcc ggc acc 225
Met Ala Leu Pro Thr Lys Ser Ser Ile Leu Asp Leu Ser Ser Gly Thr
1 5 10 15
cca tgc acc aga tct cca gag gaa agt cac gag gct tgg gca cag tgc 273
Pro Cys Thr Arg Ser Pro Glu Glu Ser His Glu Ala Trp Ala Gln Cys
20 25 30
aaa gat gct ggc agg cag cta ccc gag tac aag gca gtg gtg gtg ggt 321
Lys Asp Ala Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly
35 40 45
gca agt ggt gtt ggt aaa agt gct ctc acc atc cag atg act cac caa 369
Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Met Thr His Gln
50 55 60
tgc ttc gtg aaa gac cat gac ccc act atc caa gat tcc tac tgg aag 417
Cys Phe Val Lys Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys
65 70 75 80
gaa gtg gcc agg gac aac gga ggc tac att cta aat gtt ctg gat aca 465
Glu Val Ala Arg Asp Asn Gly Gly Tyr Ile Leu Asn Val Leu Asp Thr
85 90 95
tct ggg cag gat att cac cgg gct ctg cgt gac cag tgc ttg gca tct 513
Ser Gly Gln Asp Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Ser
100 105 110
ggt gat ggt gtg ctg ggc gtc ttt gct ctt gac gac ccc tcg tct ctg 561
Gly Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu
115 120 125
gac cag ttg cag cag ata tgg tcc acc tgg acc cct cac cac aag cag 609
Asp Gln Leu Gln Gln Ile Trp Ser Thr Trp Thr Pro His His Lys Gln
130 135 140
cct ctg gta cta gtg ggc aac aag tgt gac ctg gtg acc act gct gga 657
Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly
145 150 155 160
gat gct cat gct gcc gca gcc ctc ctt gct cac aag ttg ggg gcc ccc 705
Asp Ala His Ala Ala Ala Ala Leu Leu Ala His Lys Leu Gly Ala Pro
165 170 175
ttg gtg aag acc tca gcc aag acg cgg caa ggt gtg gag gaa gcc ttt 753
Leu Val Lys Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe
180 185 190
gcc ctg ctt gtc cat gag att cag agg gcc cag gag gct gtg gcc gaa 801
Ala Leu Leu Val His Glu Ile Gln Arg Ala Gln Glu Ala Val Ala Glu
195 200 205
tca agc aag aag acc cga cac cag aaa gcc gtg tgt agc tgt ggc tgc 849
Ser Ser Lys Lys Thr Arg His Gln Lys Ala Val Cys Ser Cys Gly Cys
210 215 220
tct gta gcc tgaagatctt tgtctagcaa attgaccctt gtctcatgtc 898

```



## 701049\_sequence\_listing.txt

Ser Val Ala  
225

aagggtgacaa ttctcttgta ataagatctc cctctccgac caagttacca cagacatctt 958  
tttattgtca tttggtgaga agttacgtgg taacatggga catccctcat tgactgtgtt 1018  
ttatgaaact ctatgcaaaa ttaaataaat gttttcagga ttcaaagctt cctttatacc 1078

<210> 18  
<211> 227  
<212> PRT  
<213> Mus musculus

<400> 18  
Met Ala Leu Pro Thr Lys Ser Ser Ile Leu Asp Leu Ser Ser Gly Thr  
1 5 10 15  
Pro Cys Thr Arg Ser Pro Glu Glu Ser His Glu Ala Trp Ala Gln Cys  
20 25 30  
Lys Asp Ala Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly  
35 40 45  
Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Met Thr His Gln  
50 55 60  
Cys Phe Val Lys Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys  
65 70 75 80  
Glu Val Ala Arg Asp Asn Gly Gly Tyr Ile Leu Asn Val Leu Asp Thr  
85 90 95  
Ser Gly Gln Asp Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Ser  
100 105 110  
Gly Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu  
115 120 125  
Asp Gln Leu Gln Gln Ile Trp Ser Thr Trp Thr Pro His His Lys Gln  
130 135 140  
Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly  
145 150 155 160  
Asp Ala His Ala Ala Ala Ala Leu Leu Ala His Lys Leu Gly Ala Pro  
165 170 175  
Leu Val Lys Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe  
180 185 190  
Ala Leu Leu Val His Glu Ile Gln Arg Ala Gln Glu Ala Val Ala Glu  
195 200 205  
Ser Ser Lys Lys Thr Arg His Gln Lys Ala Val Cys Ser Cys Gly Cys  
210 215 220  
Ser Val Ala  
225

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<210> 19
<211> 1266
<212> DNA
<213> Homo sapiens
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[illegible]

## 701049\_sequence\_listing.txt

Gly Ala His Phe Val Glu Thr Ser Ala Lys Thr Arg Gln Gly Val Glu  
 175 180 185

gag gcc ttt tcc ctg ctg gtc cat gag atc cag agg gtc cag gag gcc 866  
 Glu Ala Phe Ser Leu Leu Val His Glu Ile Gln Arg Val Gln Glu Ala  
 190 195 200 205

atg gcg aag gag ccc atg gca agg tcc tgt agg gag aag acc cgg cac 914  
 Met Ala Lys Glu Pro Met Ala Arg Ser Cys Arg Glu Lys Thr Arg His  
 210 215 220

cag aag gcc acc tgc cac tgt ggc tgc tct gtg gcc tgaaggtctt 960  
 Gln Lys Ala Thr Cys His Cys Gly Cys Ser Val Ala  
 225 230

ggccaagaaa ttagacctt tccccaggcc aggggtgattg ttcatttgac atgagacccc 1020

tgaggcaact agctttgagg gacacatcag gtatactagg gaaagatgga catctctctt 1080

gttttcactt ggtgaggggc tttttggtaa catgggagtg cctaagtgtg cttttgttat 1140

gtcaagttga aagattttgt gcaaaattaa ataaatggtg ttttgggttt caaagctgcc 1200

tccatgccga gtgttggtg ggtgggagtg agactgggta gaatgttact tgagttgtga 1260

gaattc 1266

<210> 20  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Glu Leu Pro Thr Lys Pro Gly Thr Phe Asp Leu Gly Leu Ala Thr  
 1 5 10 15

Trp Ser Pro Ser Phe Gln Gly Glu Thr His Arg Ala Gln Ala Arg Arg  
 20 25 30

Arg Asp Val Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly  
 35 40 45

Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu Asn His Gln  
 50 55 60

Cys Phe Val Glu Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys  
 65 70 75 80

Glu Leu Thr Leu Asp Ser Gly Asp Cys Ile Leu Asn Val Leu Asp Thr  
 85 90 95

Ala Gly Gln Ala Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Val  
 100 105 110

Cys Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu  
 115 120 125

Ile Gln Leu Gln Gln Ile Trp Ala Thr Trp Gly Pro His Pro Ala Gln  
 130 135 140

Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly  
 145 150 155 160

## 701049\_sequence\_listing.txt

Asp Ala His Ala Ala Ala Ala Leu Ala His Ser Trp Gly Ala His  
 165 170 175  
 Phe Val Glu Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe  
 180 185 190  
 Ser Leu Leu Val His Glu Ile Gln Arg Val Gln Glu Ala Met Ala Lys  
 195 200 205  
 Glu Pro Met Ala Arg Ser Cys Arg Glu Lys Thr Arg His Gln Lys Ala  
 210 215 220  
 Thr Cys His Cys Gly Cys Ser Val Ala  
 225 230

<210> 21  
 <211> 1063  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (177)..(872)

<400> 21  
 gatacaaatt cgaatgtagg tgctaggcgc gcttggtgta gagtgtttgt taggggagac 60  
 tgatggaatc cacagtccaa tgagtacagg gcctgtcctc cgtgtggcag cttcaccg 120  
 gagttgctgg cctggctgcc tacctgcttt cctgagatcc agggactttt cccaga atg 179  
 Met  
 1  
 gct ttg ggt gac ctc ctg ctg tct gtc ctc tct gcc cag gaa atg aat 227  
 Ala Leu Gly Asp Leu Leu Leu Ser Val Leu Ser Ala Gln Glu Met Asn  
 5 10 15  
 gcc ctt cgt ggc cag gtg ggc ggg gac gtc aat gtg gag atg gac gcc 275  
 Ala Leu Arg Gly Gln Val Gly Gly Asp Val Asn Val Glu Met Asp Ala  
 20 25 30  
 gcc ccc ggt gtg gac ctg agc cgc atc ctg aac gag atg cgg gat cag 323  
 Ala Pro Gly Val Asp Leu Ser Arg Ile Leu Asn Glu Met Arg Asp Gln  
 35 40 45  
 tat gag aag atg gcg gag aag aac cgc aag gat gct gag gaa tgg ttc 371  
 Tyr Glu Lys Met Ala Glu Lys Asn Arg Lys Asp Ala Glu Glu Trp Phe  
 50 55 60 65  
 ttc acc aag aca gag gag ctg aac cga gaa gtg gcc acc aac acg gag 419  
 Phe Thr Lys Thr Glu Glu Leu Asn Arg Glu Val Ala Thr Asn Thr Glu  
 70 75 80  
 gcc ctg cag agc agc cgg aca gag atc acg gag ctc cgc cgc tct gtg 467  
 Ala Leu Gln Ser Ser Arg Thr Glu Ile Thr Glu Leu Arg Arg Ser Val  
 85 90 95  
 cag aac ctg gag att gag ctg cag tcc cag ctc agc atg aaa gca tca 515  
 Gln Asn Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ser  
 100 105 110

701049\_sequence\_listing.txt

ctg gag aac agc ctg gca gag aca gag gcg cgc tat ggg gcc cag ctg	563
Leu Glu Asn Ser Leu Ala Glu Thr Glu Ala Arg Tyr Gly Ala Gln Leu	
115 120 125	
gcg cag ctg cag ggc ctc att agc agt gtg gaa cag cag ctg tgt gag	611
Ala Gln Leu Gln Gly Leu Ile Ser Ser Val Glu Gln Gln Leu Cys Glu	
130 135 140 145	
ctg cgt tgt gac atg gaa agg cag aat cat gag tac cag gtg ctg ctg	659
Leu Arg Cys Asp Met Glu Arg Gln Asn His Glu Tyr Gln Val Leu Leu	
150 155 160	
gat gtg aag acc cga ctg gag cag gag atc gcc acc tac cgc cgt ctg	707
Asp Val Lys Thr Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Arg Leu	
165 170 175	
ctg gag ggc gag gac gcc cac ctg gct act caa tac tcc tca tcc ctg	755
Leu Glu Gly Glu Asp Ala His Leu Ala Thr Gln Tyr Ser Ser Ser Leu	
180 185 190	
gct tcg cag ccc tcc cga gaa ggc atg gtg acc agc cgc cag gtg cgc	803
Ala Ser Gln Pro Ser Arg Glu Gly Met Val Thr Ser Arg Gln Val Arg	
195 200 205	
acc att gtg gag gaa gtc cag gat ggt aag gtg ttt tcc tcc aga gag	851
Thr Ile Val Glu Glu Val Gln Asp Gly Lys Val Phe Ser Ser Arg Glu	
210 215 220 225	
cag gag cac cgc tcc acc cac tgaggcccct gtctgcgtat gatagcccag	902
Gln Glu His Arg Ser Thr His	
230	
gcccaggacc ttaggctgca gctccctgca tctactgcca agcctgaact cctatgagct	962
agctgttgcc ttctgtgttt gctttgtgct gccccttaca gagaggcccc ttgggttgac	1022
cccagaaatt gctaataaag ctttgaagaa gtctgatacct t	1063
<210> 22	
<211> 232	
<212> PRT	
<213> Mus musculus	
<400> 22	
Met Ala Leu Gly Asp Leu Leu Leu Ser Val Leu Ser Ala Gln Glu Met	
1 5 10 15	
Asn Ala Leu Arg Gly Gln Val Gly Gly Asp Val Asn Val Glu Met Asp	
20 25 30	
Ala Ala Pro Gly Val Asp Leu Ser Arg Ile Leu Asn Glu Met Arg Asp	
35 40 45	
Gln Tyr Glu Lys Met Ala Glu Lys Asn Arg Lys Asp Ala Glu Glu Trp	
50 55 60	
Phe Phe Thr Lys Thr Glu Glu Leu Asn Arg Glu Val Ala Thr Asn Thr	
65 70 75 80	
Glu Ala Leu Gln Ser Ser Arg Thr Glu Ile Thr Glu Leu Arg Arg Ser	
85 90 95	

701049\_sequence\_listing.txt

Val Gln Asn Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala  
100 105 110  
Ser Leu Glu Asn Ser Leu Ala Glu Thr Glu Ala Arg Tyr Gly Ala Gln  
115 120 125  
Leu Ala Gln Leu Gln Gly Leu Ile Ser Ser Val Glu Gln Gln Leu Cys  
130 135 140  
Glu Leu Arg Cys Asp Met Glu Arg Gln Asn His Glu Tyr Gln Val Leu  
145 150 155 160  
Leu Asp Val Lys Thr Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Arg  
165 170 175  
Leu Leu Glu Gly Glu Asp Ala His Leu Ala Thr Gln Tyr Ser Ser Ser  
180 185 190  
Leu Ala Ser Gln Pro Ser Arg Glu Gly Met Val Thr Ser Arg Gln Val  
195 200 205  
Arg Thr Ile Val Glu Glu Val Gln Asp Gly Lys Val Phe Ser Ser Arg  
210 215 220  
Glu Gln Glu His Arg Ser Thr His  
225 230

<210> 23  
<211> 1670  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (139)..(1401)

<400> 23  
gacaccctca accccatcat cccaggccct cataggctcc atccagcatt acgtcctcat 60  
ccctacctac gggttctgac gaccctgctg tcacaccgc catcccttgg acgcagaccc 120  
ttctagccga ttacatca atg ggt tcc cgg gag aca cct tct tct tgc tct 171  
Met Gly Ser Arg Glu Thr Pro Ser Ser Cys Ser  
1 5 10  
aag acc ctt gaa acc ttg gac ctg gag act tcc gac agc tct agc cct 219  
Lys Thr Leu Glu Thr Leu Asp Leu Glu Thr Ser Asp Ser Ser Pro  
15 20 25  
gat gct gac agt cct ctg gaa gag caa tgg ctg aaa tcc tcc cca gcc 267  
Asp Ala Asp Ser Pro Leu Glu Glu Gln Trp Leu Lys Ser Ser Pro Ala  
30 35 40  
ctg aag gag gac agt gtg gat gtg gta ctg gaa gac tgc aaa gag cct 315  
Leu Lys Glu Asp Ser Val Asp Val Val Leu Glu Asp Cys Lys Glu Pro  
45 50 55  
ctg tcc ccc tcc tcg cct ccg aca ggc aga gag atg atc agg tac gaa 363  
Leu Ser Pro Ser Ser Pro Pro Thr Gly Arg Glu Met Ile Arg Tyr Glu  
60 65 70 75

## 701049\_sequence\_listing.txt

gtc	aaa	gtg	aac	cga	cgg	agc	att	gaa	gac	atc	tgc	ctc	tgc	tgt	gga	411
Val	Lys	Val	Asn	Arg	Arg	Ser	Ile	Glu	Asp	Ile	Cys	Leu	Cys	Cys	Gly	
				80					85					90		
act	ctc	cag	gtg	tac	act	cgg	cac	ccc	ttg	ttt	gag	gga	ggg	tta	tgt	459
Thr	Leu	Gln	Val	Tyr	Thr	Arg	His	Pro	Leu	Phe	Glu	Gly	Gly	Leu	Cys	
			95					100					105			
gcc	cca	tgt	aag	gat	aag	ttc	ctg	gag	tcc	ctc	ttc	ctg	tat	gat	gat	507
Ala	Pro	Cys	Lys	Asp	Lys	Phe	Leu	Glu	Ser	Leu	Phe	Leu	Tyr	Asp	Asp	
		110					115					120				
gat	gga	cac	cag	agt	tac	tgc	acc	atc	tgc	tgt	tcc	ggg	ggt	acc	ctg	555
Asp	Gly	His	Gln	Ser	Tyr	Cys	Thr	Ile	Cys	Cys	Ser	Gly	Gly	Thr	Leu	
	125					130					135					
ttc	atc	tgt	gag	agc	ccc	gac	tgt	acc	aga	tgc	tac	tgt	ttc	gag	tgt	603
Phe	Ile	Cys	Glu	Ser	Pro	Asp	Cys	Thr	Arg	Cys	Tyr	Cys	Phe	Glu	Cys	
					145					150					155	
gtg	gac	atc	ctg	gtg	ggc	ccc	ggg	acc	tca	gag	agg	atc	aat	gcc	atg	651
Val	Asp	Ile	Leu	Val	Gly	Pro	Gly	Thr	Ser	Glu	Arg	Ile	Asn	Ala	Met	
				160					165					170		
gcc	tgc	tgg	gtt	tgc	ttc	ctg	tgc	ctg	ccc	ttc	tca	cgg	agt	gga	ctg	699
Ala	Cys	Trp	Val	Cys	Phe	Leu	Cys	Leu	Pro	Phe	Ser	Arg	Ser	Gly	Leu	
			175					180					185			
ctg	cag	agg	cgc	aag	agg	tgg	cgg	cac	cag	ctg	aag	gcc	ttc	cat	gat	747
Leu	Gln	Arg	Arg	Lys	Arg	Trp	Arg	His	Gln	Leu	Lys	Ala	Phe	His	Asp	
		190					195					200				
caa	gag	gga	gcg	ggc	cct	atg	gag	ata	tac	aag	aca	gtg	tct	gca	tgg	795
Gln	Glu	Gly	Ala	Gly	Pro	Met	Glu	Ile	Tyr	Lys	Thr	Val	Ser	Ala	Trp	
	205					210					215					
aag	aga	cag	cca	gtg	cgg	gta	ctg	agc	ctt	ttt	aga	aat	att	gat	aaa	843
Lys	Arg	Gln	Pro	Val	Arg	Val	Leu	Ser	Leu	Phe	Arg	Asn	Ile	Asp	Lys	
	220				225					230					235	
gta	cta	aag	agt	ttg	ggc	ttt	ttg	gaa	agc	ggt	tct	ggt	tct	ggg	gga	891
Val	Leu	Lys	Ser	Leu	Gly	Phe	Leu	Glu	Ser	Gly	Ser	Gly	Ser	Gly	Gly	
				240					245					250		
gga	acg	ctg	aag	tac	gtg	gaa	gat	gtc	aca	aat	gtc	gtg	agg	aga	gac	939
Gly	Thr	Leu	Lys	Tyr	Val	Glu	Asp	Val	Thr	Asn	Val	Val	Arg	Arg	Asp	
			255					260					265			
gtg	gag	aaa	tgg	ggc	ccc	ttt	gac	ctg	gtg	tac	ggc	tcg	acg	cag	ccc	987
Val	Glu	Lys	Trp	Gly	Pro	Phe	Asp	Leu	Val	Tyr	Gly	Ser	Thr	Gln	Pro	
		270					275					280				
cta	ggc	agc	tct	tgt	gat	cgc	tgt	ccc	ggc	tgg	tac	atg	ttc	cag	ttc	1035
Leu	Gly	Ser	Ser	Cys	Asp	Arg	Cys	Pro	Gly	Trp	Tyr	Met	Phe	Gln	Phe	
	285					290					295					
cac	cgg	atc	ctg	cag	tat	gcg	ctg	cct	cgc	cag	gag	agt	cag	cgg	ccc	1083
His	Arg	Ile	Leu	Gln	Tyr	Ala	Leu	Pro	Arg	Gln	Glu	Ser	Gln	Arg	Pro	
					305					310					315	
ttc	ttc	tgg	ata	ttc	atg	gac	aat	ctg	ctg	ctg	act	gag	gat	gac	caa	1131
Phe	Phe	Trp	Ile	Phe	Met	Asp	Asn	Leu	Leu	Leu	Thr	Glu	Asp	Asp	Gln	

## 701049\_sequence\_listing.txt

```

320                                325                                330
gag aca act acc cgc ttc ctt cag aca gag gct gtg acc ctc cag gat 1179
Glu Thr Thr Thr Arg Phe Leu Gln Thr Glu Ala Val Thr Leu Gln Asp
335                                340                                345

gtc cgt ggc aga gac tac cag aat gct atg cgg gtg tgg agc aac att 1227
Val Arg Gly Arg Asp Tyr Gln Asn Ala Met Arg Val Trp Ser Asn Ile
350                                355                                360

cca ggg ctg aag agc aag cat gcg ccc ctg acc cca aag gaa gaa gag 1275
Pro Gly Leu Lys Ser Lys His Ala Pro Leu Thr Pro Lys Glu Glu Glu
365                                370                                375

tat ctg caa gcc caa gtc aga agc agg agc aag ctg gac gcc ccg aaa 1323
Tyr Leu Gln Ala Gln Val Arg Ser Arg Ser Lys Leu Asp Ala Pro Lys
380                                385                                390

gtt gac ctc ctg gtg aag aac tgc ctt ctc ccg ctg aga gag tac ttc 1371
Val Asp Leu Leu Val Lys Asn Cys Leu Leu Pro Leu Arg Glu Tyr Phe
400                                405                                410

aag tat ttt tct caa aac tca ctt cct ctt tagaaatgaa tcaccataag 1421
Lys Tyr Phe Ser Gln Asn Ser Leu Pro Leu
415                                420

atgaaagtct ttcctagaac cagggcagat ttcttcctaa ggtctcttcc ctccacagtt 1481
ttctctgggt tgctttcagg ccttcgggtt tctctcctgt ttgattgcca ggatgcctct 1541
gtgcagctca ctttgcgggg tgggaggtgc ctacggctct gcacaagttc ccggtgggat 1601
aacctgccat gtttctctga aactgtgtgt acctgttgtg aagtttttca aatatatcat 1661
aggattggtt 1670

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<210> 24  
 <211> 421  
 <212> PRT  
 <213> Mus musculus

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<400> 24
Met Gly Ser Arg Glu Thr Pro Ser Ser Cys Ser Lys Thr Leu Glu Thr
 1      5      10      15
Leu Asp Leu Glu Thr Ser Asp Ser Ser Ser Pro Asp Ala Asp Ser Pro
20      25      30
Leu Glu Glu Gln Trp Leu Lys Ser Ser Pro Ala Leu Lys Glu Asp Ser
35      40      45
Val Asp Val Val Leu Glu Asp Cys Lys Glu Pro Leu Ser Pro Ser Ser
50      55      60
Pro Pro Thr Gly Arg Glu Met Ile Arg Tyr Glu Val Lys Val Asn Arg
65      70      75      80
Arg Ser Ile Glu Asp Ile Cys Leu Cys Cys Gly Thr Leu Gln Val Tyr
85      90      95
Thr Arg His Pro Leu Phe Glu Gly Gly Leu Cys Ala Pro Cys Lys Asp
100      105      110

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## 701049\_sequence\_listing.txt

Lys Phe Leu Glu Ser Leu Phe Leu Tyr Asp Asp Asp Gly His Gln Ser  
 115 120 125  
 Tyr Cys Thr Ile Cys Cys Ser Gly Gly Thr Leu Phe Ile Cys Glu Ser  
 130 135 140  
 Pro Asp Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ile Leu Val  
 145 150 155 160  
 Gly Pro Gly Thr Ser Glu Arg Ile Asn Ala Met Ala Cys Trp Val Cys  
 165 170 175  
 Phe Leu Cys Leu Pro Phe Ser Arg Ser Gly Leu Leu Gln Arg Arg Lys  
 180 185 190  
 Arg Trp Arg His Gln Leu Lys Ala Phe His Asp Gln Glu Gly Ala Gly  
 195 200 205  
 Pro Met Glu Ile Tyr Lys Thr Val Ser Ala Trp Lys Arg Gln Pro Val  
 210 215 220  
 Arg Val Leu Ser Leu Phe Arg Asn Ile Asp Lys Val Leu Lys Ser Leu  
 225 230 235 240  
 Gly Phe Leu Glu Ser Gly Ser Gly Ser Gly Gly Gly Thr Leu Lys Tyr  
 245 250 255  
 Val Glu Asp Val Thr Asn Val Val Arg Arg Asp Val Glu Lys Trp Gly  
 260 265 270  
 Pro Phe Asp Leu Val Tyr Gly Ser Thr Gln Pro Leu Gly Ser Ser Cys  
 275 280 285  
 Asp Arg Cys Pro Gly Trp Tyr Met Phe Gln Phe His Arg Ile Leu Gln  
 290 295 300  
 Tyr Ala Leu Pro Arg Gln Glu Ser Gln Arg Pro Phe Phe Trp Ile Phe  
 305 310 315 320  
 Met Asp Asn Leu Leu Leu Thr Glu Asp Asp Gln Glu Thr Thr Thr Arg  
 325 330 335  
 Phe Leu Gln Thr Glu Ala Val Thr Leu Gln Asp Val Arg Gly Arg Asp  
 340 345 350  
 Tyr Gln Asn Ala Met Arg Val Trp Ser Asn Ile Pro Gly Leu Lys Ser  
 355 360 365  
 Lys His Ala Pro Leu Thr Pro Lys Glu Glu Glu Tyr Leu Gln Ala Gln  
 370 375 380  
 Val Arg Ser Arg Ser Lys Leu Asp Ala Pro Lys Val Asp Leu Leu Val  
 385 390 395 400  
 Lys Asn Cys Leu Leu Pro Leu Arg Glu Tyr Phe Lys Tyr Phe Ser Gln  
 405 410 415  
 Asn Ser Leu Pro Leu  
 420

## 701049\_sequence\_listing.txt

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 <211> 1705  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (485)..(1645)

<400> 25  
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 actccaccct gagggcccca tcctctgaac cccaatcccc cagccccact gagctcttaa 120  
 ccctccccac ctgagggttc cttttccctg cccgtcccc agcttcctag ctccccaccc 180  
 caagtgacct cccgcagctc ctgcgccctc ccaactgcaaa ccggcactga agggctgccc 240  
 cgcccccgcc cctccccgcc cccgcgggac acgcccagat tctttgcccc catagcctgg 300  
 tgacctctgg ccaccgctg tcccagggtg gcctggatcc ttccagctca ttctttgcct 360  
 gcgccgtccc tcgttccatg gcccagtcct ccccggggac cctgagcctg gaagccccgg 420  
 accactggaa ccttgaaccc accagctggc tgtacccgga gccgtggcag cagccctcat 480  
 cccc atg gcg gcc atc cca gcc ctg gac cca gag gcc gag ccc agc atg 529  
       Met Ala Ala Ile Pro Ala Leu Asp Pro Glu Ala Glu Pro Ser Met  
       1                  5                  10                  15  
 gac gtg att ttg gtg gga tcc agt gag ctc tca agc tcc gtt tca ccc 577  
 Asp Val Ile Leu Val Gly Ser Ser Glu Leu Ser Ser Ser Val Ser Pro  
                   20                  25                  30  
 ggg aca ggc aga gat ctt att gca tat gaa gtc aag gct aac cag cga 625  
 Gly Thr Gly Arg Asp Leu Ile Ala Tyr Glu Val Lys Ala Asn Gln Arg  
                   35                  40                  45  
 aat ata gaa gac atc tgc atc tgc tgc gga agt ctc cag gtt cac aca 673  
 Asn Ile Glu Asp Ile Cys Ile Cys Cys Gly Ser Leu Gln Val His Thr  
                   50                  55                  60  
 cag cac cct ctg ttt gag gga ggg atc tgc gcc cca tgt aag gac aag 721  
 Gln His Pro Leu Phe Glu Gly Gly Ile Cys Ala Pro Cys Lys Asp Lys  
                   65                  70                  75  
 ttc ctg gat gcc ctc ttc ctg tac gac gat gac ggg tac caa tcc tac 769  
 Phe Leu Asp Ala Leu Phe Leu Tyr Asp Asp Asp Gly Tyr Gln Ser Tyr  
                   80                  85                  90                  95  
 tgc tcc atc tgc tgc tcc gga gag acg ctg ctc atc tgc gga aac cct 817  
 Cys Ser Ile Cys Cys Ser Gly Glu Thr Leu Leu Ile Cys Gly Asn Pro  
                   100                  105                  110  
 gat tgc acc cga tgc tac tgc ttc gag tgt gtg gat agc ctg gtc ggc 865  
 Asp Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ser Leu Val Gly  
                   115                  120                  125  
 ccc ggg acc tcg ggg aag gtg cac gcc atg agc aac tgg gtg tgc tac 913  
 Pro Gly Thr Ser Gly Lys Val His Ala Met Ser Asn Trp Val Cys Tyr  
                   130                  135                  140  
 ctg tgc ctg ccg tcc tcc cga agc ggg ctg ctg cag cgt cgg agg aag 961

## 701049\_sequence\_listing.txt

Leu	Cys 145	Leu	Pro	Ser	Ser	Arg 150	Ser	Gly	Leu	Leu	Gln 155	Arg	Arg	Arg	Lys	
tgg	cgc	agc	cag	ctc	aag	gcc	ttc	tac	gac	cga	gag	tcg	gag	aat	ccc	1009
Trp	Arg	Ser	Gln	Leu	Lys 165	Ala	Phe	Tyr	Asp	Arg 170	Glu	Ser	Glu	Asn	Pro 175	
160																
ctt	gag	atg	ttc	gaa	acc	gtg	cct	gtg	tgg	agg	aga	cag	cca	gtc	cgg	1057
Leu	Glu	Met	Phe	Glu 180	Thr	Val	Pro	Val	Trp 185	Arg	Arg	Gln	Pro	Val 190	Arg	
gtg	ctg	tcc	ctt	ttt	gaa	gac	atc	aag	aaa	gag	ctg	acg	agt	ttg	ggc	1105
Val	Leu	Ser	Leu 195	Phe	Glu	Asp	Ile	Lys 200	Lys	Glu	Leu	Thr	Ser 205	Leu	Gly	
ttt	ttg	gaa	agt	ggt	tct	gac	ccg	gga	caa	ctg	aag	cat	gtg	gtt	gat	1153
Phe	Leu	Glu 210	Ser	Gly	Ser	Asp	Pro 215	Gly	Gln	Leu	Lys	His 220	Val	Val	Asp	
gtc	aca	gac	aca	gtg	agg	aag	gat	gtg	gag	gag	tgg	gga	ccc	ttc	gat	1201
Val	Thr 225	Asp	Thr	Val	Arg	Lys 230	Asp	Val	Glu	Glu	Trp 235	Gly	Pro	Phe	Asp	
ctt	gtg	tac	ggc	gcc	aca	gct	ccc	ctg	ggc	cac	acc	tgt	gac	cgt	cct	1249
Leu	Val	Tyr	Gly	Ala	Thr 245	Ala	Pro	Leu	Gly	His 250	Thr	Cys	Asp	Arg	Pro 255	
240																
ccc	agc	tgg	tac	ctg	ttc	cag	ttc	cac	cgg	ttc	ctg	cag	tac	gca	cgg	1297
Pro	Ser	Trp	Tyr	Leu 260	Phe	Gln	Phe	His	Arg 265	Phe	Leu	Gln	Tyr	Ala 270	Arg	
ccc	aag	cca	ggc	agc	ccc	agg	ccc	ttc	ttc	tgg	atg	ttc	gtg	gac	aat	1345
Pro	Lys	Pro	Gly 275	Ser	Pro	Arg	Pro	Phe 280	Phe	Trp	Met	Phe	Val 285	Asp	Asn	
ctg	gtg	ctg	aac	aag	gaa	gac	ctg	gac	gtc	gca	tct	cgc	ttc	ctg	gag	1393
Leu	Val	Leu 290	Asn	Lys	Glu	Asp	Leu 295	Asp	Val	Ala	Ser	Arg 300	Phe	Leu	Glu	
atg	gag	cca	gtc	acc	atc	cca	gat	gtc	cac	ggc	gga	tcc	ttg	cag	aat	1441
Met	Glu 305	Pro	Val	Thr	Ile	Pro 310	Asp	Val	His	Gly 315	Gly	Ser	Leu	Gln	Asn	
gct	gtc	cgc	gtg	tgg	agc	aac	atc	cca	gcc	ata	agg	agc	agc	agg	cac	1489
Ala	Val	Arg	Val	Trp	Ser 325	Asn	Ile	Pro	Ala	Ile 330	Arg	Ser	Ser	Arg	His 335	
320																
tgg	gct	ctg	gtt	tcg	gaa	gaa	gaa	ttg	tcc	ctg	ctg	gcc	cag	aac	aag	1537
Trp	Ala	Leu	Val	Ser 340	Glu	Glu	Glu	Leu	Ser 345	Leu	Leu	Ala	Gln	Asn 350	Lys	
cag	agc	tcg	aag	ctc	gcg	gcc	aag	tgg	ccc	acc	aag	ctg	gtg	aag	aac	1585
Gln	Ser	Ser	Lys 355	Leu	Ala	Ala	Lys	Trp 360	Pro	Thr	Lys	Leu	Val 365	Lys	Asn	
tgc	ttt	ctc	ccc	cta	aga	gaa	tat	ttc	aag	tat	ttt	tca	aca	gaa	ctc	1633
Cys	Phe	Leu 370	Pro	Leu	Arg	Glu	Tyr 375	Phe	Lys	Tyr	Phe	Ser 380	Thr	Glu	Leu	
act	tcc	tct	tta	taa	atg	agtc	act	tata	ctgt	ga	agaaaa	aag	act	tttc	ccta	1685
Thr	Ser 385	Ser	Leu													

gaacaaaggc aactttcctc

1705

&lt;210&gt; 26

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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Val  Ile  Leu  Val  Gly  Ser  Ser  Glu  Leu  Ser  Ser  Ser  Val  Ser  Pro  Gly
 20          25          30
Thr  Gly  Arg  Asp  Leu  Ile  Ala  Tyr  Glu  Val  Lys  Ala  Asn  Gln  Arg  Asn
 35          40          45
Ile  Glu  Asp  Ile  Cys  Ile  Cys  Cys  Gly  Ser  Leu  Gln  Val  His  Thr  Gln
 50          55          60
His  Pro  Leu  Phe  Glu  Gly  Gly  Ile  Cys  Ala  Pro  Cys  Lys  Asp  Lys  Phe
 65          70          75
Leu  Asp  Ala  Leu  Phe  Leu  Tyr  Asp  Asp  Asp  Gly  Tyr  Gln  Ser  Tyr  Cys
 85          90          95
Ser  Ile  Cys  Cys  Ser  Gly  Glu  Thr  Leu  Leu  Ile  Cys  Gly  Asn  Pro  Asp
100          105          110
Cys  Thr  Arg  Cys  Tyr  Cys  Phe  Glu  Cys  Val  Asp  Ser  Leu  Val  Gly  Pro
115          120          125
Gly  Thr  Ser  Gly  Lys  Val  His  Ala  Met  Ser  Asn  Trp  Val  Cys  Tyr  Leu
130          135          140
Cys  Leu  Pro  Ser  Ser  Arg  Ser  Gly  Leu  Leu  Gln  Arg  Arg  Arg  Lys  Trp
145          150          155
Arg  Ser  Gln  Leu  Lys  Ala  Phe  Tyr  Asp  Arg  Glu  Ser  Glu  Asn  Pro  Leu
165          170          175
Glu  Met  Phe  Glu  Thr  Val  Pro  Val  Trp  Arg  Arg  Gln  Pro  Val  Arg  Val
180          185          190
Leu  Ser  Leu  Phe  Glu  Asp  Ile  Lys  Lys  Glu  Leu  Thr  Ser  Leu  Gly  Phe
195          200          205
Leu  Glu  Ser  Gly  Ser  Asp  Pro  Gly  Gln  Leu  Lys  His  Val  Val  Asp  Val
210          215          220
Thr  Asp  Thr  Val  Arg  Lys  Asp  Val  Glu  Glu  Trp  Gly  Pro  Phe  Asp  Leu
225          230          235
Val  Tyr  Gly  Ala  Thr  Ala  Pro  Leu  Gly  His  Thr  Cys  Asp  Arg  Pro  Pro
245          250          255
Ser  Trp  Tyr  Leu  Phe  Gln  Phe  His  Arg  Phe  Leu  Gln  Tyr  Ala  Arg  Pro
260          265          270
Lys  Pro  Gly  Ser  Pro  Arg  Pro  Phe  Phe  Trp  Met  Phe  Val  Asp  Asn  Leu
275          280          285

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701049\_sequence\_listing.txt

Val Leu Asn Lys Glu Asp Leu Asp Val Ala Ser Arg Phe Leu Glu Met  
 290 295 300  
 Glu Pro Val Thr Ile Pro Asp Val His Gly Gly Ser Leu Gln Asn Ala  
 305 310 315 320  
 Val Arg Val Trp Ser Asn Ile Pro Ala Ile Arg Ser Ser Arg His Trp  
 325 330 335  
 Ala Leu Val Ser Glu Glu Glu Leu Ser Leu Leu Ala Gln Asn Lys Gln  
 340 345 350  
 Ser Ser Lys Leu Ala Ala Lys Trp Pro Thr Lys Leu Val Lys Asn Cys  
 355 360 365  
 Phe Leu Pro Leu Arg Glu Tyr Phe Lys Tyr Phe Ser Thr Glu Leu Thr  
 370 375 380  
 Ser Ser Leu  
 385

<210> 27  
 <211> 1560  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (147)..(1367)

<400> 27  
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 atctcctctg tgagagaagg gccagg atg ttc gag gtc ctg gtg ctg aag att 173  
 Met Phe Glu Val Leu Val Leu Lys Ile  
 1 5  
 gaa gat cca ggt tgc ttc tgg gta att ata aaa gga tgt agt cat ttt 221  
 Glu Asp Pro Gly Cys Phe Trp Val Ile Ile Lys Gly Cys Ser His Phe  
 10 15 20 25  
 tta gaa caa gaa gtt gac tac caa aaa cta aac act gcc atg aat gac 269  
 Leu Glu Gln Glu Val Asp Tyr Gln Lys Leu Asn Thr Ala Met Asn Asp  
 30 35 40  
 ttc tat aac agc atg tgt cag gac gta gaa atg aaa cca tta atg ctg 317  
 Phe Tyr Asn Ser Met Cys Gln Asp Val Glu Met Lys Pro Leu Met Leu  
 45 50 55  
 gaa gaa ggg cag gtg tgt gtg gtg tac tgc cag gag ctg aag tgc tgg 365  
 Glu Glu Gly Gln Val Cys Val Val Tyr Cys Gln Glu Leu Lys Cys Trp  
 60 65 70  
 tgc agg gct ctg att aag tcc atc atc tct tct gca gac cat tac ctg 413  
 Cys Arg Ala Leu Ile Lys Ser Ile Ile Ser Ser Ala Asp His Tyr Leu  
 75 80 85  
 gca gag tgt ttc ctg gtc gat ttt gcc aag tat att cca gta aaa tct 461  
 Ala Glu Cys Phe Leu Val Asp Phe Ala Lys Tyr Ile Pro Val Lys Ser  
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## 701049\_sequence\_listing.txt

90	95	100	105	
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gca aaa aaa ttc aga ctt tac ggt aca aag cct gtg aca ttg cac att	Phe 125	Arg Leu Tyr Gly Thr 130	Lys Pro Val Thr Leu His Ile 135	557
gac ttc tgt gaa gac aat gct gag att gta cct gcc aca aaa tgg gac	Cys 140	Glu Asp Asn Ala Glu Ile Val Pro Ala Thr Lys Trp Asp 150		605
agt gca gcc atc cag tac ttt cag aac ctt cta aga gca act acc caa	Ala 155	Ala Ile Gln Tyr Phe 160	Leu Leu Arg Ala Thr Thr Gln 165	653
gtg gaa gca aaa cta tgt gcg gtg gaa gaa gat act ttt gag gtt tac	Glu 170	Ala Lys Leu Cys 175	Ala Val Glu Glu Asp Thr Phe Glu Val Tyr 180 185	701
ctt tat gca aca ata aaa aat gaa aaa gtt tgt gtt aat gat gac cta	Ala Thr 190	Ile Lys Asn Glu Lys Val 195	Cys Val Asn Asp Asp Leu 200	749
gtt gca aag aat ttt gct tat tat gtg tca cca atg ggg aat aaa aac	Ala Lys Asn Phe Ala Tyr Tyr Val 210	Ala Ser Pro Met Gly Asn Lys Asn 215		797
ctc aat cct ttg gag aaa ccc agg cag agt ctc aat tcg gtg acc tgc	Asn Pro 220	Leu Glu Lys Pro Arg 225	Gln Ser Leu Asn Ser Val Thr Cys 230	845
tcc agt aag ctc agc cca tca ctt act ctg tgg cca atg ctt cta caa	Ser Ser 235	Leu Lys Ser Pro Ser 240	Thr Leu Trp Pro Met Leu Leu Gln 245	893
gga aaa gac tat cac aga atg gaa aat aaa gct cta aac tat aag gat	Lys Asp Tyr His Arg 255	Met Glu Asn Lys Ala 260	Leu Asn Tyr Lys Asp 265	941
tcc ttg aca gac tcg cct aaa atg atg ctt gag aag cag cag cag agc	Leu Thr Asp Ser 270	Pro Lys Met Met Leu 275	Glu Lys Gln Gln Gln Ser 280	989
ctc cct tta aag cac acg gag aag tgt act gaa tct tct gtg tac tgg	Pro Leu Lys His Thr Glu Lys Cys 290	Thr Thr Glu Ser Ser Val 295	Tyr Trp 300	1037
cca acc aaa aga ggc ata acc ata tat gct gat cca gat gtt cca tca	Pro Thr Lys Arg Gly Ile Thr Ile Tyr 305	Ala Asp Pro Asp Val Pro Ser 310		1085
gta agt ggg tct agc cag agg ccg aat gag aag cca ctg cggttg act	Val Ser Gly Ser Ser Gln Arg 320	Pro Asn Glu Lys Pro 325	Leu Arg Leu Thr 330	1133
gaa aag aaa gac tgt gac gag aag aac ggc tgt gta aaa tta ctg cag	Glu Lys Lys Asp Cys Asp 335	Glu Lys Asn Gly Cys 340	Val Lys Leu Leu Gln 345	1181
ttt cta aat cct gat cct ttg aga gct gat ggg acc tca gac ctg cac				1229

701049\_sequence\_listing.txt

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Phe Leu Asn Pro Asp Pro Leu Arg Ala Asp Gly Thr Ser Asp Leu His
      350      355      360
cag ttg cag aag gtg aag ctg ggc aca ctg cag cct ggg gtg gtg ctc 1277
Gln Leu Gln Lys Val Lys Leu Gly Thr Leu Gln Pro Gly Val Val Leu
      365      370      375
cgg aac agg atc gag ccc tgc cta acc ctg gag aaa tca cct ctg tcg 1325
Arg Asn Arg Ile Glu Pro Cys Leu Thr Leu Glu Lys Ser Pro Leu Ser
      380      385      390
gca gac ctg aag aag gtg aac atg ttc tta aag cca gac tcc 1367
Ala Asp Leu Lys Lys Val Asn Met Phe Leu Lys Pro Asp Ser
      395      400      405
tgacgacatg ccagcccttt ccaacacaga gtgttgcttt gttttgcttt gtctgttctg 1427
ttctaagagt gacggggatg aaatacaggg ctttgcgcgt cctgggcatg cattcatcac 1487
tgaaccatac cccaattcca taggaggatt ttaaataaac acttctaagg ctacattgca 1547
gaattcttgc tcc 1560

```

<210> 28  
 <211> 407  
 <212> PRT  
 <213> Mus musculus

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<400> 28
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  1      5      10      15
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      20      25      30
Gln Lys Leu Asn Thr Ala Met Asn Asp Phe Tyr Asn Ser Met Cys Gln
      35      40      45
Asp Val Glu Met Lys Pro Leu Met Leu Glu Glu Gly Gln Val Cys Val
      50      55      60
Val Tyr Cys Gln Glu Leu Lys Cys Trp Cys Arg Ala Leu Ile Lys Ser
      65      70      75      80
Ile Ile Ser Ser Ala Asp His Tyr Leu Ala Glu Cys Phe Leu Val Asp
      85      90      95
Phe Ala Lys Tyr Ile Pro Val Lys Ser Lys Asn Ile Arg Val Ala Val
      100      105      110
Glu Ser Phe Met Gln Leu Pro Tyr Arg Ala Lys Lys Phe Arg Leu Tyr
      115      120      125
Gly Thr Lys Pro Val Thr Leu His Ile Asp Phe Cys Glu Asp Asn Ala
      130      135      140
Glu Ile Val Pro Ala Thr Lys Trp Asp Ser Ala Ala Ile Gln Tyr Phe
      145      150      155      160
Gln Asn Leu Leu Arg Ala Thr Thr Gln Val Glu Ala Lys Leu Cys Ala
      165      170      175

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701049\_sequence\_listing.txt

Val Glu Glu Asp Thr Phe Glu Val Tyr Leu Tyr Ala Thr Ile Lys Asn  
180 185 190

Glu Lys Val Cys Val Asn Asp Asp Leu Val Ala Lys Asn Phe Ala Tyr  
195 200 205

Tyr Val Ser Pro Met Gly Asn Lys Asn Leu Asn Pro Leu Glu Lys Pro  
210 215 220

Arg Gln Ser Leu Asn Ser Val Thr Cys Ser Ser Lys Leu Ser Pro Ser  
225 230 235 240

Leu Thr Leu Trp Pro Met Leu Leu Gln Gly Lys Asp Tyr His Arg Met  
245 250 255

Glu Asn Lys Ala Leu Asn Tyr Lys Asp Ser Leu Thr Asp Ser Pro Lys  
260 265 270

Met Met Leu Glu Lys Gln Gln Gln Ser Leu Pro Leu Lys His Thr Glu  
275 280 285

Lys Cys Thr Glu Ser Ser Val Tyr Trp Pro Thr Lys Arg Gly Ile Thr  
290 295 300

Ile Tyr Ala Asp Pro Asp Val Pro Ser Val Ser Gly Ser Ser Gln Arg  
305 310 315 320

Pro Asn Glu Lys Pro Leu Arg Leu Thr Glu Lys Lys Asp Cys Asp Glu  
325 330 335

Lys Asn Gly Cys Val Lys Leu Leu Gln Phe Leu Asn Pro Asp Pro Leu  
340 345 350

Arg Ala Asp Gly Thr Ser Asp Leu His Gln Leu Gln Lys Val Lys Leu  
355 360 365

Gly Thr Leu Gln Pro Gly Val Val Leu Arg Asn Arg Ile Glu Pro Cys  
370 375 380

Leu Thr Leu Glu Lys Ser Pro Leu Ser Ala Asp Leu Lys Lys Val Asn  
385 390 395 400

Met Phe Leu Lys Pro Asp Ser  
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<210> 29  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (97)..(1167)

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Met Asn Asp Phe Tyr Asn  
1 5



## 701049\_sequence\_listing.txt

agc Ser	acg Thr	tgt Cys	caa Gln 10	gat Asp	ata Ile	gaa Glu	ata Ile	aaa Lys 15	ccc Pro	tta Leu	aca Thr	ttg Leu	gaa Glu 20	gaa Glu	gga Gly	162
cag Gln	gtg Val	tgt Cys 25	gtg Val	gtc Val	tat Tyr	tgt Cys	gag Glu 30	gag Glu	cta Leu	aag Lys	tgc Cys	tgg Trp 35	tgc Cys	agg Arg	gcc Ala	210
att Ile	gtc Val 40	aaa Lys	tca Ser	att Ile	acg Thr	tct Ser 45	tcc Ser	gca Ala	gac Asp	cag Gln	tac Tyr 50	ctg Leu	gca Ala	gaa Glu	tgt Cys	258
ttc Phe 55	ctt Leu	gtg Val	gac Asp	ttt Phe	gcc Ala 60	aag Lys	aac Asn	att Ile	cca Pro	gtc Val 65	aaa Lys	tct Ser	aaa Lys	agc Ser	atc Ile 70	306
cga Arg	gtt Val	gta Val	gta Val	gaa Glu 75	tcg Ser	ttt Phe	atg Met	cag Gln	ctt Leu 80	ccc Pro	tat Tyr	aga Arg	gca Ala	aaa Lys 85	aaa Lys	354
ttc Phe	agc Ser	ctg Leu	tac Tyr 90	tgc Cys	aca Thr	aag Lys	cct Pro	gtc Val 95	aca Thr	tta Leu	cac His	att Ile	gac Asp 100	ttc Phe	tgc Cys	402
cga Arg	gac Asp	agt Ser 105	act Thr	gac Asp	att Ile	gtg Val	cct Pro 110	gcc Ala	aag Lys	aag Lys	tgg Trp	gac Asp 115	aat Asn	gca Ala	gct Ala	450
att Ile 120	cag Gln	tac Tyr	ttt Phe	cag Gln	aac Asn	ctt Leu 125	ctg Leu	aaa Lys	gca Ala	act Thr	acc Thr 130	cag Gln	gtg Val	gaa Glu	gcc Ala	498
aga Arg 135	tta Leu	tgt Cys	gct Ala	gtg Val	gaa Glu 140	gaa Glu	gat Asp	aca Thr	ttt Phe	gag Glu 145	gtt Val	tac Tyr	ctt Leu	tat Tyr	gta Val 150	546
act Thr	ata Ile	aaa Lys	gat Asp	gaa Glu 155	aaa Lys	gtt Val	tgt Cys	gtt Val	aat Asn 160	gat Asp	gat Asp	ctt Leu	gtt Val	gca Ala 165	aag Lys	594
aac Asn	tat Tyr	gct Ala	tgt Cys 170	tat Tyr	atg Met	tca Ser	cct Pro	aca Thr 175	aag Lys	aat Asn	aaa Lys	aac Asn	ctt Leu 180	gat Asp	tat Tyr	642
tta Leu	gaa Glu 185	aaa Lys	cca Pro	aga Arg	ttg Leu	aat Asn	ata Ile 190	aaa Lys	tca Ser	gca Ala	ccc Pro	tcc Ser 195	ttc Phe	aat Asn	aaa Lys	690
ctc Leu 200	aat Asn	cca Pro	gca Ala	ctt Leu	aca Thr	ctc Leu 205	tgg Trp	cca Pro	atg Met	ttt Phe	ttg Leu 210	caa Gln	gga Gly	aaa Lys	gat Asp	738
gtt Val 215	caa Gln	gga Gly	atg Met	gaa Glu	gat Asp 220	tca Ser	cat His	ggt Gly	gta Val	aat Asn 225	ttt Phe	ccg Pro	gca Ala	caa Gln	tct Ser 230	786
ctg Leu	caa Gln	cat His	aca Thr	tgg Trp 235	tgc Cys	aag Lys	ggt Gly	att Ile	gtc Val 240	ggt Gly	gac Asp	ctc Leu	agg Arg	cca Pro 245	aca Thr	834
gcc Ala	aca Thr	gca Ala	cag Gln 250	gac Asp	aaa Lys	gct Ala	gta Val	aaa Lys 255	tgt Cys	aat Asn	atg Met	gat Asp	tca Ser 260	ttg Leu	aga Arg	882

## 701049\_sequence\_listing.txt

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gat tca cct aaa gac aaa tct gaa aag aaa cac cat tgc atc tct tta 930
Asp Ser Pro Lys Asp Lys Ser Glu Lys Lys His His Cys Ile Ser Leu
265 270 275

aaa gat aca aat aag cgt gtt gaa tcc tca gtg tac tgg cca gca aaa 978
Lys Asp Thr Asn Lys Arg Val Glu Ser Ser Val Tyr Trp Pro Ala Lys
280 285 290

aga ggc ata acc ata tat gct gat cca gat gta cca gaa gca agt gct 1026
Arg Gly Ile Thr Ile Tyr Ala Asp Pro Asp Val Pro Glu Ala Ser Ala
295 300 305 310

tta agt cag aag tca aat gag aaa cct ctt aga ttg act gag aag aaa 1074
Leu Ser Gln Lys Ser Asn Glu Lys Pro Leu Arg Leu Thr Glu Lys Lys
315 320 325

gaa tat gat gag aag aat agc tgt gtg aaa tta ctg cag ttt tta aat 1122
Glu Tyr Asp Glu Lys Asn Ser Cys Val Lys Leu Leu Gln Phe Leu Asn
330 335 340

cct gat cct ttg aga gct gac gga atc tct gat ctc cag cag act 1167
Pro Asp Pro Leu Arg Ala Asp Gly Ile Ser Asp Leu Gln Gln Thr
345 350 355

tgagattaga agagaaactc cttagatggg ggacttaacc tgaagacatc ctttagaaa 1227
cgatcgaatg gattgttgct tctgagaaat tgttccttgt tttttggata ataaacgatc 1287
ttccttttgg taaa 1301

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<210> 30
<211> 357
<212> PRT
<213> Homo sapiens

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<400> 30
Met Asn Asp Phe Tyr 5 Asn Ser Thr Cys Gln Asp Ile Glu Ile Lys Pro
1 10 15

Leu Thr Leu Glu Glu Gly Gln Val Cys Val Val Tyr Cys Glu Glu Leu
20 25 30

Lys Cys Trp Cys Arg Ala Ile Val Lys Ser Ile Thr Ser Ser Ala Asp
35 40 45

Gln Tyr Leu Ala Glu Cys Phe Leu Val Asp Phe Ala Lys Asn Ile Pro
50 55 60

Val Lys Ser Lys Ser Ile Arg Val Val Val Glu Ser Phe Met Gln Leu
65 70 75 80

Pro Tyr Arg Ala Lys Lys Phe Ser Leu Tyr Cys Thr Lys Pro Val Thr
85 90 95

Leu His Ile Asp Phe Cys Arg Asp Ser Thr Asp Ile Val Pro Ala Lys
100 105 110

Lys Trp Asp Asn Ala Ala Ile Gln Tyr Phe Gln Asn Leu Leu Lys Ala
115 120 125

Thr Thr Gln Val Glu Ala Arg Leu Cys Ala Val Glu Glu Asp Thr Phe

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701049\_sequence\_listing.txt

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130                               135                               140
Glu Val Tyr Leu Tyr Val Thr Ile Lys Asp Glu Lys Val Cys Val Asn
145                               150                               155                               160
Asp Asp Leu Val Ala Lys Asn Tyr Ala Cys Tyr Met Ser Pro Thr Lys
165                               170                               175
Asn Lys Asn Leu Asp Tyr Leu Glu Lys Pro Arg Leu Asn Ile Lys Ser
180                               185                               190
Ala Pro Ser Phe Asn Lys Leu Asn Pro Ala Leu Thr Leu Trp Pro Met
195                               200                               205
Phe Leu Gln Gly Lys Asp Val Gln Gly Met Glu Asp Ser His Gly Val
210                               215                               220
Asn Phe Pro Ala Gln Ser Leu Gln His Thr Trp Cys Lys Gly Ile Val
225                               230                               235
Gly Asp Leu Arg Pro Thr Ala Thr Ala Gln Asp Lys Ala Val Lys Cys
245                               250                               255
Asn Met Asp Ser Leu Arg Asp Ser Pro Lys Asp Lys Ser Glu Lys Lys
260                               265                               270
His His Cys Ile Ser Leu Lys Asp Thr Asn Lys Arg Val Glu Ser Ser
275                               280                               285
Val Tyr Trp Pro Ala Lys Arg Gly Ile Thr Ile Tyr Ala Asp Pro Asp
290                               295                               300
Val Pro Glu Ala Ser Ala Leu Ser Gln Lys Ser Asn Glu Lys Pro Leu
305                               310                               315
Arg Leu Thr Glu Lys Lys Glu Tyr Asp Glu Lys Asn Ser Cys Val Lys
325                               330                               335
Leu Leu Gln Phe Leu Asn Pro Asp Pro Leu Arg Ala Asp Gly Ile Ser
340                               345                               350
Asp Leu Gln Gln Thr
355

```

```

<210> 31
<211> 1280
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (122)..(1219)

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gaggaggcta gaccgctgag ctgcgcaccc cagaggctgc tctaccctgg ctgagacgac 120
c atg cag cct tat caa cgg ctt ctg gcg ctt ggc ttc ctt ctg tta acc 169
Met Gln Pro Tyr Gln Arg Leu Leu Ala Leu Gly Phe Leu Leu Leu Thr
1 5 10 15

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## 701049\_sequence\_listing.txt

ctg	ccc	tgg	ggc	cag	aca	tcc	gag	ttt	caa	gac	tct	gac	ctt	ttg	cag	217
Leu	Pro	Trp	Gly	Gln	Thr	Ser	Glu	Phe	Gln	Asp	Ser	Asp	Leu	Leu	Gln	
			20					25					30			
ttt	ctg	gga	tta	gag	aaa	gcg	cct	tca	cct	cac	agg	ttc	caa	cct	gtg	265
Phe	Leu	Gly	Leu	Glu	Lys	Ala	Pro	Ser	Pro	His	Arg	Phe	Gln	Pro	Val	
		35					40					45				
cct	cgc	gtc	tta	agg	aaa	atc	atc	cgg	gct	cga	gaa	gcc	gct	gca	gcc	313
Pro	Arg	Val	Leu	Arg	Lys	Ile	Ile	Arg	Ala	Arg	Glu	Ala	Ala	Ala	Ala	
	50					55					60					
agt	ggg	gcc	tcg	cag	gac	tta	tgc	tac	gtg	aag	gag	ctg	ggt	gtt	cgt	361
Ser	Gly	Ala	Ser	Gln	Asp	Leu	Cys	Tyr	Val	Lys	Glu	Leu	Gly	Val	Arg	
65					70					75					80	
ggg	aac	ctg	ctt	cag	ctt	ctc	cca	gac	cag	ggg	ttt	ttc	ctt	aat	aca	409
Gly	Asn	Leu	Leu	Gln	Leu	Leu	Pro	Asp	Gln	Gly	Phe	Phe	Leu	Asn	Thr	
				85					90					95		
cag	aaa	cct	ttc	caa	gat	ggc	tcc	tgt	ctc	cag	aag	gtc	ctc	tat	ttt	457
Gln	Lys	Pro	Phe	Gln	Asp	Gly	Ser	Cys	Leu	Gln	Lys	Val	Leu	Tyr	Phe	
			100					105					110			
aac	ttg	tct	gcc	atc	aaa	gaa	aag	gca	aag	ttg	acc	atg	gcc	cag	ctg	505
Asn	Leu	Ser	Ala	Ile	Lys	Glu	Lys	Ala	Lys	Leu	Thr	Met	Ala	Gln	Leu	
		115					120					125				
act	cta	gac	ttg	ggg	ccc	agg	tcc	tac	tat	aac	ctg	cga	cca	gag	ctg	553
Thr	Leu	Asp	Leu	Gly	Pro	Arg	Ser	Tyr	Tyr	Asn	Leu	Arg	Pro	Glu	Leu	
	130					135					140					
gtg	gtt	gct	ctg	tct	gtg	gtt	cag	gac	cgg	ggc	gtg	tgg	ggg	cga	tcc	601
Val	Val	Ala	Leu	Ser	Val	Val	Gln	Asp	Arg	Gly	Val	Trp	Gly	Arg	Ser	
145					150					155					160	
cac	cct	aag	gtg	ggc	aga	ttg	ctt	ttt	ctg	cgg	tct	gtc	cct	ggg	cct	649
His	Pro	Lys	Val	Gly	Arg	Leu	Leu	Phe	Leu	Arg	Ser	Val	Pro	Gly	Pro	
				165					170					175		
caa	ggt	cag	ctc	cag	ttc	aac	ctg	cag	ggt	gcg	ctt	aag	gat	tgg	agc	697
Gln	Gly	Gln	Leu	Gln	Phe	Asn	Leu	Gln	Gly	Ala	Leu	Lys	Asp	Trp	Ser	
			180					185					190			
agc	aac	cga	ctg	aag	aat	ttg	gac	tta	cac	tta	gag	att	ttg	gtc	aaa	745
Ser	Asn	Arg	Leu	Lys	Asn	Leu	Asp	Leu	His	Leu	Glu	Ile	Leu	Val	Lys	
		195					200					205				
gag	gac	aga	tac	tcc	agg	gta	act	gtc	cag	ccc	gag	aac	ccc	tgt	gac	793
Glu	Asp	Arg	Tyr	Ser	Arg	Val	Thr	Val	Gln	Pro	Glu	Asn	Pro	Cys	Asp	
	210					215					220					
ccg	ctg	ctc	cgc	tct	cta	cat	gcc	tcg	ctg	ctg	gtg	gta	acc	ctc	aat	841
Pro	Leu	Leu	Arg	Ser	Leu	His	Ala	Ser	Leu	Leu	Val	Val	Thr	Leu	Asn	
225					230					235					240	
cct	aaa	cac	tgt	cat	cct	tct	tcc	aga	aaa	agg	agg	gcg	gcc	atc	tct	889
Pro	Lys	His	Cys	His	Pro	Ser	Ser	Arg	Lys	Arg	Arg	Ala	Ala	Ile	Ser	
				245					250					255		
gtc	ccc	aag	ggt	ttc	tgt	agg	aac	ttc	tgc	cac	cgt	cat	cag	ctg	ttc	937
Val	Pro	Lys	Gly	Phe	Cys	Arg	Asn	Phe	Cys	His	Arg	His	Gln	Leu	Phe	

## 701049\_sequence\_listing.txt

260  
 atc aac ttc cag gac ctg ggt tgg cac aag tgg gtc atc gcc cct aag 985  
 Ile Asn Phe Gln Asp Leu Gly Trp His Lys Trp Val Ile Ala Pro Lys  
 275 280 285  
 ggg ttc atg gca aat tac tgt cat gga gag tgc ccc ttc tca atg acc 1033  
 Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Met Thr  
 290 295 300  
 acg tat tta aat agt tcc aat tat gct ttc atg cag gct ctg atg cat 1081  
 Thr Tyr Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His  
 305 310 315 320  
 atg gct gac ccc aag gtc ccc aag gct gtc tgt gtc ccc acc aag ctc 1129  
 Met Ala Asp Pro Lys Val Pro Lys Ala Val Cys Val Pro Thr Lys Leu  
 325 330 335  
 tcg ccc atc tcc atg ctc tat cag gat agt gat aag aac gtc att ctc 1177  
 Ser Pro Ile Ser Met Leu Tyr Gln Asp Ser Asp Lys Asn Val Ile Leu  
 340 345 350  
 cga cat tat gaa gac atg gta gtc gat gag tgt ggg tgt ggg 1219  
 Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly  
 355 360 365  
 tagtctcggg actaggctag gagtgtgctt agggtaaadc ctttaataaaa actaccaccc 1279  
 c 1280

<210> 32  
 <211> 366  
 <212> PRT  
 <213> Mus musculus

<400> 32  
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 Leu Pro Trp Gly Gln Thr Ser Glu Phe Gln Asp Ser Asp Leu Leu Gln  
 20 25 30  
 Phe Leu Gly Leu Glu Lys Ala Pro Ser Pro His Arg Phe Gln Pro Val  
 35 40 45  
 Pro Arg Val Leu Arg Lys Ile Ile Arg Ala Arg Glu Ala Ala Ala Ala  
 50 55 60  
 Ser Gly Ala Ser Gln Asp Leu Cys Tyr Val Lys Glu Leu Gly Val Arg  
 65 70 75 80  
 Gly Asn Leu Leu Gln Leu Leu Pro Asp Gln Gly Phe Phe Leu Asn Thr  
 85 90 95  
 Gln Lys Pro Phe Gln Asp Gly Ser Cys Leu Gln Lys Val Leu Tyr Phe  
 100 105 110  
 Asn Leu Ser Ala Ile Lys Glu Lys Ala Lys Leu Thr Met Ala Gln Leu  
 115 120 125  
 Thr Leu Asp Leu Gly Pro Arg Ser Tyr Tyr Asn Leu Arg Pro Glu Leu  
 130 135 140

701049\_sequence\_listing.txt

Val Val Ala Leu Ser Val Val Gln Asp Arg Gly Val Trp Gly Arg Ser  
 145 150 155 160  
 His Pro Lys Val Gly Arg Leu Leu Phe Leu Arg Ser Val Pro Gly Pro  
 165 170 175  
 Gln Gly Gln Leu Gln Phe Asn Leu Gln Gly Ala Leu Lys Asp Trp Ser  
 180 185 190  
 Ser Asn Arg Leu Lys Asn Leu Asp Leu His Leu Glu Ile Leu Val Lys  
 195 200 205  
 Glu Asp Arg Tyr Ser Arg Val Thr Val Gln Pro Glu Asn Pro Cys Asp  
 210 215 220  
 Pro Leu Leu Arg Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn  
 225 230 235 240  
 Pro Lys His Cys His Pro Ser Ser Arg Lys Arg Arg Ala Ala Ile Ser  
 245 250 255  
 Val Pro Lys Gly Phe Cys Arg Asn Phe Cys His Arg His Gln Leu Phe  
 260 265 270  
 Ile Asn Phe Gln Asp Leu Gly Trp His Lys Trp Val Ile Ala Pro Lys  
 275 280 285  
 Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Met Thr  
 290 295 300  
 Thr Tyr Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His  
 305 310 315 320  
 Met Ala Asp Pro Lys Val Pro Lys Ala Val Cys Val Pro Thr Lys Leu  
 325 330 335  
 Ser Pro Ile Ser Met Leu Tyr Gln Asp Ser Asp Lys Asn Val Ile Leu  
 340 345 350  
 Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly  
 355 360 365

<210> 33  
 <211> 1224  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (37)..(1128)

<400> 33  
 ggagctctcc ccggtctgac agccactcca gaggcc atg ctt cgt ttc ttg cca 54  
 Met Leu Arg Phe Leu Pro  
 1 5

gat ttg gct ttc agc ttc ctg tta att ctg gct ttg ggc cag gca gtc 102  
 Asp Leu Ala Phe Ser Phe Leu Leu Ile Leu Ala Leu Gly Gln Ala Val  
 10 15 20

## 701049\_sequence\_listing.txt

caa ttt caa gaa tat gtc ttt ctc caa ttt ctg ggc tta gat aag gcg Gln Phe Gln Glu Tyr Val Phe Leu Gln Phe Leu Gly Leu Asp Lys Ala 25 30 35	150
cct tca ccc cag aag ttc caa cct gtg cct tat atc ttg aag aaa att Pro Ser Pro Gln Lys Phe Gln Pro Val Pro Tyr Ile Leu Lys Lys Ile 40 45 50	198
ttc cag gat cgc gag gca gca gcg acc act ggg gtc tcc cga gac tta Phe Gln Asp Arg Glu Ala Ala Ala Thr Thr Gly Val Ser Arg Asp Leu 55 60 65 70	246
tgc tac gta aag gag ctg ggc gtc cgc ggg aat gta ctt cgc ttt ctc Cys Tyr Val Lys Glu Leu Gly Val Arg Gly Asn Val Leu Arg Phe Leu 75 80 85	294
cca gac caa ggt ttc ttt ctt tac cca aag aaa att tcc caa gct tcc Pro Asp Gln Gly Phe Phe Leu Tyr Pro Lys Lys Ile Ser Gln Ala Ser 90 95 100	342
tcc tgc ctg cag aag ctc ctc tac ttt aac ctg tct gcc atc aaa gaa Ser Cys Leu Gln Lys Leu Leu Tyr Phe Asn Leu Ser Ala Ile Lys Glu 105 110 115	390
agg gaa cag ttg aca ttg gcc cag ctg ggc ctg gac ttg ggg ccc aat Arg Glu Gln Leu Thr Leu Ala Gln Leu Gly Leu Asp Leu Gly Pro Asn 120 125 130	438
tct tac tat aac ctg gga cca gag ctg gaa ctg gct ctg ttc ctg gtt Ser Tyr Tyr Asn Leu Gly Pro Glu Leu Glu Leu Ala Leu Phe Leu Val 135 140 145 150	486
cag gag cct cat gtg tgg ggc cag acc acc cct aag cca ggt aaa atg Gln Glu Pro His Val Trp Gly Gln Thr Thr Pro Lys Pro Gly Lys Met 155 160 165	534
ttt gtg ttg cgg tca gtc cca tgg cca caa ggt gct gtt cac ttc aac Phe Val Leu Arg Ser Val Pro Trp Pro Gln Gly Ala Val His Phe Asn 170 175 180	582
ctg ctg gat gta gct aag gat tgg aat gac aac ccc cgg aaa aat ttc Leu Leu Asp Val Ala Lys Asp Trp Asn Asp Asn Pro Arg Lys Asn Phe 185 190 195	630
ggg tta ttc ctg gag ata ctg gtc aaa gaa gat aga gac tca ggg gtg Gly Leu Phe Leu Glu Ile Leu Val Lys Glu Asp Arg Asp Ser Gly Val 200 205 210	678
aat ttt cag cct gaa gac acc tgt gcc aga cta aga tgc tcc ctt cat Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg Leu Arg Cys Ser Leu His 215 220 225 230	726
gct tcc ctg ctg gtg gtg act ctc aac cct gat cag tgc cac cct tct Ala Ser Leu Leu Val Val Thr Leu Asn Pro Asp Gln Cys His Pro Ser 235 240 245	774
cgg aaa agg aga gca gcc atc cct gtc ccc aag ctt tct tgt aag aac Arg Lys Arg Arg Ala Ala Ile Pro Val Pro Lys Leu Ser Cys Lys Asn 250 255 260	822
ctc tgc cac cgt cac cag cta ttc att aac ttc cgg gac ctg ggt tgg Leu Cys His Arg His Gln Leu Phe Ile Asn Phe Arg Asp Leu Gly Trp 265 270 275	870

## 701049\_sequence\_listing.txt

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cac aag tgg atc att gcc ccc aag ggg ttc atg gca aat tac tgc cat 918
His Lys Trp Ile Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His
280 285 290

gga gag tgt ccc ttc tca ctg acc atc tct ctc aac agc tcc aat tat 966
Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr
295 300 305

gct ttc atg caa gcc ctg atg cat gcc gtt gac cca gag atc ccc cag 1014
Ala Phe Met Gln Ala Leu Met His Ala Val Asp Pro Glu Ile Pro Gln
315 320 325

gct gtg tgt atc ccc acc aag ctg tct ccc att tcc atg ctc tac cag 1062
Ala Val Cys Ile Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln
330 335 340

gac aat aat gac aat gtc att cta cga cat tat gaa gac atg gta gtc 1110
Asp Asn Asn Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val
345 350 355

gat gaa tgt ggg tgt ggg taggatgtca gaaatgggaa tagaaggagt 1158
Asp Glu Cys Gly Cys Gly

gttcttaggg taaatctttt aataaaacta cctatctggt ttatgaccac ttagatcgaa 1218
atgtca 1224

<210> 34
<211> 364
<212> PRT
<213> Homo sapiens

<400> 34
Met Leu Arg Phe Leu Pro Asp Leu Ala Phe Ser Phe Leu Leu Ile Leu
1 5 10 15
Ala Leu Gly Gln Ala Val Gln Phe Gln Glu Tyr Val Phe Leu Gln Phe
20 25 30
Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln Pro Val Pro
35 40 45
Tyr Ile Leu Lys Lys Ile Phe Gln Asp Arg Glu Ala Ala Ala Thr Thr
50 55 60
Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu Leu Gly Val Arg Gly
65 70 75 80
Asn Val Leu Arg Phe Leu Pro Asp Gln Gly Phe Phe Leu Tyr Pro Lys
85 90 95
Lys Ile Ser Gln Ala Ser Ser Cys Leu Gln Lys Leu Leu Tyr Phe Asn
100 105 110
Leu Ser Ala Ile Lys Glu Arg Glu Gln Leu Thr Leu Ala Gln Leu Gly
115 120 125
Leu Asp Leu Gly Pro Asn Ser Tyr Tyr Asn Leu Gly Pro Glu Leu Glu
130 135 140

```



701049\_sequence\_listing.txt

Leu Ala Leu Phe Leu Val Gln Glu Pro His Val Trp Gly Gln Thr Thr  
145 150 155 160  
Pro Lys Pro Gly Lys Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln  
165 170 175  
Gly Ala Val His Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp  
180 185 190  
Asn Pro Arg Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu  
195 200 205  
Asp Arg Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg  
210 215 220  
Leu Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro  
225 230 235 240  
Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val Pro  
245 250 255  
Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe Ile Asn  
260 265 270  
Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro Lys Gly Phe  
275 280 285  
Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser  
290 295 300  
Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His Ala Val  
305 310 315 320  
Asp Pro Glu Ile Pro Gln Ala Val Cys Ile Pro Thr Lys Leu Ser Pro  
325 330 335  
Ile Ser Met Leu Tyr Gln Asp Asn Asn Asp Asn Val Ile Leu Arg His  
340 345 350  
Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly  
355 360

<210> 35  
<211> 1248  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (32)..(1003)

<400> 35  
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Met Asp Pro Arg Thr Trp Leu  
1 5  
agc ttc caa ggg cct cca ggt ggg cct gga atc gga cca ggc tca gag 100  
Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly Pro Gly Ser Glu  
10 15 20  
gta ttg ggg atc tcc cca tgt ccg ccc gca tac gag ttc tgc gga ggg 148  
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## 701049\_sequence\_listing.txt

Val	Leu	Gly	Ile	Ser	Pro	Cys	Pro	Pro	Ala	Tyr	Glu	Phe	Cys	Gly	Gly	
	25					30					35					
atg	gca	tac	tgt	gga	cct	cag	gtt	ggc	ctg	ggc	cta	gtc	ccc	caa	gtt	196
Met	Ala	Tyr	Cys	Gly	Pro	Gln	Val	Gly	Leu	Gly	Leu	Val	Pro	Gln	Val	
40					45			50							55	
ggc	gtg	gag	act	ttg	cag	cct	gag	ggc	cag	gca	gga	gca	cga	gtg	gaa	244
Gly	Val	Glu	Thr	Leu	Gln	Pro	Glu	Gly	Gln	Ala	Gly	Ala	Arg	Val	Glu	
				60				65						70		
agc	aac	tca	gag	gga	acc	tcc	tct	gag	ccc	tgt	gcc	gac	cgc	ccc	aat	292
Ser	Asn	Ser	Glu	Gly	Thr	Ser	Ser	Glu	Pro	Cys	Ala	Asp	Arg	Pro	Asn	
			75					80					85			
gcc	gtg	aag	ttg	gag	aag	gtg	gaa	cca	act	ccc	gag	gag	tcc	cag	gac	340
Ala	Val	Lys	Leu	Glu	Lys	Val	Glu	Pro	Thr	Pro	Glu	Glu	Ser	Gln	Asp	
		90					95				100					
atg	aaa	gcc	ctg	cag	aag	gag	cta	gaa	cag	ttt	gcc	aag	ctg	ctg	aag	388
Met	Lys	Ala	Leu	Gln	Lys	Glu	Leu	Glu	Gln	Phe	Ala	Lys	Leu	Leu	Lys	
	105					110					115					
cag	aag	agg	atc	acc	ttg	ggg	tac	acc	cag	gcc	gac	gtg	ggg	ctc	acc	436
Gln	Lys	Arg	Ile	Thr	Leu	Gly	Tyr	Thr	Gln	Ala	Asp	Val	Gly	Leu	Thr	
120					125					130					135	
ctg	ggc	gtt	ctc	ttt	gga	aag	gtg	ttc	agc	cag	acc	acc	atc	tgt	cgc	484
Leu	Gly	Val	Leu	Phe	Gly	Lys	Val	Phe	Ser	Gln	Thr	Thr	Ile	Cys	Arg	
				140					145					150		
ttc	gag	gcc	ttg	cag	ctc	agc	ctt	aag	aac	atg	tgt	aag	ctg	cgg	ccc	532
Phe	Glu	Ala	Leu	Gln	Leu	Ser	Leu	Lys	Asn	Met	Cys	Lys	Leu	Arg	Pro	
			155					160					165			
ctg	ctg	gag	aag	tgg	gtg	gag	gaa	gcc	gac	aac	aat	gag	aac	ctt	cag	580
Leu	Leu	Glu	Lys	Trp	Val	Glu	Glu	Ala	Asp	Asn	Asn	Glu	Asn	Leu	Gln	
		170					175					180				
gag	ata	tgc	aaa	tcg	gag	acc	ctg	gtg	cag	gcc	cgg	aag	aga	aag	cga	628
Glu	Ile	Cys	Lys	Ser	Glu	Thr	Leu	Val	Gln	Ala	Arg	Lys	Arg	Lys	Arg	
	185					190					195					
act	agc	att	gag	aac	cgt	gtg	agg	tgg	agt	ctg	gag	acc	atg	ttt	ctg	676
Thr	Ser	Ile	Glu	Asn	Arg	Val	Arg	Trp	Ser	Leu	Glu	Thr	Met	Phe	Leu	
200					205					210					215	
aag	tgc	ccg	aag	ccc	tcc	cta	cag	cag	atc	act	cac	atc	gcc	aat	cag	724
Lys	Cys	Pro	Lys	Pro	Ser	Leu	Gln	Gln	Ile	Thr	His	Ile	Ala	Asn	Gln	
				220					225				230			
ctt	ggg	cta	gag	aag	gat	gtg	gtt	cga	gta	tgg	ttc	tgt	aac	cgg	cgc	772
Leu	Gly	Leu	Glu	Lys	Asp	Val	Val	Arg	Val	Trp	Phe	Cys	Asn	Arg	Arg	
			235					240					245			
cag	aag	ggc	aaa	aga	tca	agt	att	gag	tat	tcc	caa	cga	gaa	gag	tat	820
Gln	Lys	Gly	Lys	Arg	Ser	Ser	Ile	Glu	Tyr	Ser	Gln	Arg	Glu	Glu	Tyr	
		250					255					260				
gag	gct	aca	ggg	aca	cct	ttc	cca	ggg	ggg	gct	gta	tcc	ttt	cct	ctg	868
Glu	Ala	Thr	Gly	Thr	Pro	Phe	Pro	Gly	Gly	Ala	Val	Ser	Phe	Pro	Leu	
	265					270					275					

701049\_sequence\_listing.txt

```

ccc cca ggt ccc cac ttt ggc acc cca ggc tat gga agc ccc cac ttc 916
Pro Pro Gly Pro His Phe Gly Thr Pro Gly Tyr Gly Ser Pro His Phe
280 285 290 295

acc aca ctc tac tca gtc cct ttt cct gag ggc gag gcc ttt ccc tct 964
Thr Thr Leu Tyr Ser Val Pro Phe Pro Glu Gly Glu Ala Phe Pro Ser
300 305 310

gtt ccc gtc act gct ctg ggc tct ccc atg cat tca aac tgaggcacca 1013
Val Pro Val Thr Ala Leu Gly Ser Pro Met His Ser Asn
315 320

gccctccctg gggatgctgt gagccaaggc aaggaggagta gacaagagaa cctggagctt 1073
tggggttaaa ttcttttact gaggagggat taaaagcaca acaggggtgg ggggtgggat 1133
ggggaaagaa gctcagtgat gctgttgatc aggagcctgg cctgtctgtc actcatcatt 1193
ttgttcttaa ataaagactg ggacacacag taaaaaaaaa aaaaaaaaaac tcgag 1248

<210> 36
<211> 324
<212> PRT
<213> Mus musculus

<400> 36
Met Asp Pro Arg Thr Trp Leu Ser Phe Gln Gly Pro Pro Gly Gly Pro
1 5 10 15
Gly Ile Gly Pro Gly Ser Glu Val Leu Gly Ile Ser Pro Cys Pro Pro
20 25 30
Ala Tyr Glu Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val Gly
35 40 45
Leu Gly Leu Val Pro Gln Val Gly Val Glu Thr Leu Gln Pro Glu Gly
50 55 60
Gln Ala Gly Ala Arg Val Glu Ser Asn Ser Glu Gly Thr Ser Ser Glu
65 70 75 80
Pro Cys Ala Asp Arg Pro Asn Ala Val Lys Leu Glu Lys Val Glu Pro
85 90 95
Thr Pro Glu Glu Ser Gln Asp Met Lys Ala Leu Gln Lys Glu Leu Glu
100 105 110
Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr Leu Gly Tyr Thr
115 120 125
Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe Gly Lys Val Phe
130 135 140
Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu Ser Leu Lys
145 150 155 160
Asn Met Cys Lys Leu Arg Pro Leu Leu Glu Lys Trp Val Glu Glu Ala
165 170 175
Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ser Glu Thr Leu Val
180 185 190

```

## 701049\_sequence\_listing.txt

Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg Val Arg Trp  
 195 200 205  
 Ser Leu Glu Thr Met Phe Leu Lys Cys Pro Lys Pro Ser Leu Gln Gln  
 210 215 220  
 Ile Thr His Ile Ala Asn Gln Leu Gly Leu Glu Lys Asp Val Val Arg  
 225 230 235 240  
 Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser Ser Ile Glu  
 245 250 255  
 Tyr Ser Gln Arg Glu Glu Tyr Glu Ala Thr Gly Thr Pro Phe Pro Gly  
 260 265 270  
 Gly Ala Val Ser Phe Pro Leu Pro Pro Gly Pro His Phe Gly Thr Pro  
 275 280 285  
 Gly Tyr Gly Ser Pro His Phe Thr Thr Leu Tyr Ser Val Pro Phe Pro  
 290 295 300  
 Glu Gly Glu Ala Phe Pro Ser Val Pro Val Thr Ala Leu Gly Ser Pro  
 305 310 315 320  
 Met His Ser Asn

<210> 37  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (43)..(1122)

<400> 37  
 ctcatttcac caggcccccg gcttggggcg ccttccttcc cc atg gcg gga cac 54  
 Met Ala Gly His  
 1  
 ctg gct tcg gat ttc gcc ttc tcg ccc cct cca ggt ggt gga ggt gat 102  
 Leu Ala Ser Asp Phe Ala Phe Ser Pro Pro Pro Gly Gly Gly Gly Asp  
 5 10 15 20  
 ggg cca ggg ggg ccg gag ccg ggc tgg gtt gat cct cgg acc tgg cta 150  
 Gly Pro Gly Gly Pro Glu Pro Gly Trp Val Asp Pro Arg Thr Trp Leu  
 25 30 35  
 agc ttc caa ggc cct cct gga ggg cca gga atc ggg ccg ggg gtt ggg 198  
 Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly Pro Gly Val Gly  
 40 45 50  
 cca ggc tct gag gtg tgg ggg att ccc cca tgc ccc ccg ccg tat gag 246  
 Pro Gly Ser Glu Val Trp Gly Ile Pro Pro Cys Pro Pro Pro Tyr Glu  
 55 60 65  
 ttc tgt ggg ggg atg gcg tac tgt ggg ccc cag gtt gga gtg ggg cta 294  
 Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val Gly Val Gly Leu  
 70 75 80

## 701049\_sequence\_listing.txt

gtg Val 85	ccc Pro	caa Gln	ggc Gly	ggc Gly	ttg Leu 90	gag Glu	acc Thr	tct Ser	cag Gln	cct Pro 95	gag Glu	ggc Gly	gaa Glu	gca Ala	gga Gly 100	342
gtc Val	ggg Gly	gtg Val	gag Glu	agc Ser 105	aac Asn	tcc Ser	gat Asp	ggg Gly	gcc Ala 110	tcc Ser	ccg Pro	gag Glu	ccc Pro	tgc Cys 115	acc Thr	390
gtc Val	acc Thr	cct Pro	ggt Gly 120	gcc Ala	gtg Val	aag Lys	ctg Leu	gag Glu 125	aag Lys	gag Glu	aag Lys	ctg Leu	gag Glu 130	caa Gln	aac Asn	438
ccg Pro	gag Glu	gag Glu 135	tcc Ser	cag Gln	gac Asp	atc Ile	aaa Lys 140	gct Ala	ctg Leu	cag Gln	aaa Lys	gaa Glu 145	ctc Leu	gag Glu	caa Gln	486
ttt Phe 150	gcc Ala	aag Lys	ctc Leu	ctg Leu	aag Lys	cag Gln 155	aag Lys	agg Arg	atc Ile	acc Thr	ctg Leu 160	gga Gly	tat Tyr	aca Thr	cag Gln	534
gcc Ala 165	gat Asp	gtg Val	ggg Gly	ctc Leu	acc Thr 170	ctg Leu	ggg Gly	gtt Val	cta Leu	ttt Phe 175	ggg Gly	aag Lys	gta Val	ttc Phe	agc Ser 180	582
caa Gln	acg Thr	acc Thr	atc Ile	tgc Cys 185	cgc Arg	ttt Phe	gag Glu	gct Ala	ctg Leu 190	cag Gln	ctt Leu	agc Ser	ttc Phe	aag Lys 195	aac Asn	630
atg Met	tgt Cys	aag Lys	ctg Leu 200	cgg Arg	ccc Pro	ttg Leu	ctg Leu	cag Gln 205	aag Lys	tgg Trp	gtg Val	gag Glu	gaa Glu 210	gct Ala	gac Asp	678
aac Asn	aat Asn	gaa Glu 215	aat Asn	ctt Leu	cag Gln	gag Glu	ata Ile 220	tgc Cys	aaa Lys	gca Ala	gaa Glu	acc Thr 225	ctc Leu	gtg Val	cag Gln	726
gcc Ala 230	cga Arg	aag Lys	aga Arg	aag Lys	cga Arg	acc Thr 235	agt Ser	atc Ile	gag Glu	aac Asn	cga Arg 240	gtg Val	aga Arg	ggc Gly	aac Asn	774
ctg Leu 245	gag Glu	aat Asn	ttg Leu	ttc Phe	ctg Leu 250	cag Gln	tgc Cys	ccg Pro	aaa Lys	ccc Pro 255	aca Thr	ctg Leu	cag Gln	cag Gln	atc Ile 260	822
agc Ser	cac His	atc Ile	gcc Ala	cag Gln 265	cag Gln	ctt Leu	ggg Gly	ctc Leu	gag Glu 270	aag Lys	gat Asp	gtg Val	gtc Val	cga Arg 275	gtg Val	870
tgg Trp	ttc Phe	tgt Cys	aac Asn 280	cgg Arg	cgc Arg	cag Gln	aag Lys	ggc Gly 285	aag Lys	cga Arg	tca Ser	agc Ser	agc Ser 290	gac Asp	tat Tyr	918
gca Ala	caa Gln	cga Arg 295	gag Glu	gat Asp	ttt Phe	gag Glu	gct Ala 300	gct Ala	ggg Gly	tct Ser	cct Pro	ttc Phe 305	tca Ser	ggg Gly	gga Gly	966
cca Pro 310	gtg Val	tcc Ser	ttt Phe	cct Pro	ctg Leu	gcc Ala 315	cca Pro	ggg Gly	ccc Pro	cat His	ttt Phe 320	ggt Gly	acc Thr	cca Pro	ggc Gly	1014
tat Tyr 325	ggg Gly	agc Ser	cct Pro	cac His	ttc Phe 330	act Thr	gca Ala	ctg Leu	tac Tyr	tcc Ser 335	tcg Ser	gtc Val	cct Pro	ttc Phe	cct Pro 340	1062

701049\_sequence\_listing.txt

gag ggg gaa gcc ttt ccc cct gtc tct gtc acc act ctg ggc tct ccc 1110  
Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr Thr Leu Gly Ser Pro  
345 350 355

atg cat tca aac tgaggtgcct gcccttctag gaatggggga cagggggagg 1162  
Met His Ser Asn  
360

ggaggagcta gggaaagaaa acctggagtt tgtgccaggg tttttggatt aagttcttca 1222

ttcactaagg aaggaattgg gaacacaaag ggtgggggca ggggagtttg gggcaactgg 1282

ttggagggaa ggtgaagttc aatgatgctc ttgattttaa tcccacatca tgtatcactt 1342

ttttcttaaa taaagaagct tgggacaca 1371

<210> 38

<211> 360

<212> PRT

<213> Homo sapiens

<400> 38

Met Ala Gly His Leu Ala Ser Asp Phe Ala Phe Ser Pro Pro Pro Gly  
1 5 10 15

Gly Gly Gly Asp Gly Pro Gly Gly Pro Glu Pro Gly Trp Val Asp Pro  
20 25 30

Arg Thr Trp Leu Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly  
35 40 45

Pro Gly Val Gly Pro Gly Ser Glu Val Trp Gly Ile Pro Pro Cys Pro  
50 55 60

Pro Pro Tyr Glu Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val  
65 70 75 80

Gly Val Gly Leu Val Pro Gln Gly Gly Leu Glu Thr Ser Gln Pro Glu  
85 90 95

Gly Glu Ala Gly Val Gly Val Glu Ser Asn Ser Asp Gly Ala Ser Pro  
100 105 110

Glu Pro Cys Thr Val Thr Pro Gly Ala Val Lys Leu Glu Lys Glu Lys  
115 120 125

Leu Glu Gln Asn Pro Glu Glu Ser Gln Asp Ile Lys Ala Leu Gln Lys  
130 135 140

Glu Leu Glu Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr Leu  
145 150 155 160

Gly Tyr Thr Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe Gly  
165 170 175

Lys Val Phe Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu  
180 185 190

Ser Phe Lys Asn Met Cys Lys Leu Arg Pro Leu Leu Gln Lys Trp Val  
195 200 205

701049\_sequence\_listing.txt

Glu Glu Ala Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ala Glu  
 210 215 220  
 Thr Leu Val Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg  
 225 230 235 240  
 Val Arg Gly Asn Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro Thr  
 245 250 255  
 Leu Gln Gln Ile Ser His Ile Ala Gln Gln Leu Gly Leu Glu Lys Asp  
 260 265 270  
 Val Val Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser  
 275 280 285  
 Ser Ser Asp Tyr Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser Pro  
 290 295 300  
 Phe Ser Gly Gly Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His Phe  
 305 310 315 320  
 Gly Thr Pro Gly Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser Ser  
 325 330 335  
 Val Pro Phe Pro Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr Thr  
 340 345 350  
 Leu Gly Ser Pro Met His Ser Asn  
 355 360

<210> 39  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 39  
 agggctctgct actgagatgc tctg

24

<210> 40  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 40  
 aggcaggtct tcagaggaag ggcg

24

<210> 41  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

701049\_sequence\_listing.txt

<400> 41  
cgggctgtag acctgtctgc attctg 26

<210> 42  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 42  
ggtccttctg tctcatcctc gagagt 26

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 43  
accaaggtca ccgcatccaa 20

<210> 44  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:primer

<400> 44  
cttcaccaag atttccgatg 20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 45  
gaatggtgga ctagcttttg 20

<210> 46  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 46  
tgccatgaat gtcgatatgc ag 22



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<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 47
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<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 48
gcggccgcct ttacgggtca cgagggtcac              30

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 49
tgtggccagt gtttggttct ggcggg                26

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 50
ctcgaggact cgccattcta gccaag                26

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